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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:32 ; Search time 11.7198 Seconds
(without alignments)
1087.222 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139
Sequence: 1 AVGMGLGAMFLGLGAGSGTMCATSWALTV 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	269	2	AAY22833
2	139	100.0	269	5	ABG68304
3	139	100.0	269	6	ABU57711
4	139	100.0	649	2	AAW44250
5	139	100.0	865	2	AAW43072
6	131	94.2	669	6	ABP73114
7	131	94.2	669	6	ABP73117
8	131	94.2	669	6	ABP73122
9	131	94.2	669	6	ABP73120
10	131	94.2	844	6	ABP73115
11	131	94.2	844	6	ABP73112
12	131	94.2	844	6	ABP73118
13	131	94.2	844	6	ABP73121
14	131	94.2	844	6	ABP73111
15	130	93.5	791	9	ADK39690
16	130	93.5	883	4	AB82761
17	130	93.5	883	9	ADM38347
18	130	93.5	883	9	ADY27998
19	130	93.5	883	9	ABE10654
20	130	93.5	883	9	ABE10552
21	129	92.8	267	2	AAY22831
22	129	92.8	267	5	ABG68302
23	129	92.8	267	6	ABU57709
24	129	92.8	855	9	ADK39676

25	128	92.1	269	2	AAY22851	Aay22851	SEQ ID NO
26	128	92.1	269	5	ABG68322	Abg68322	Envelope
27	128	92.1	269	6	ABU57729	Abu57729	Human imm
28	127	91.4	269	2	AAY22816	Aay22816	SEQ ID NO
29	127	91.4	269	5	ABG68287	Abg68287	Envelope
30	127	91.4	269	6	ABU57694	Abu57694	Human imm
31	127	91.4	855	2	AAW43069	Aaw43069	HIV-1 gp1
32	126	90.6	269	2	AAY22836	Aay22836	SEQ ID NO
33	126	90.6	269	2	AAY22848	Aay22848	SEQ ID NO
34	126	90.6	269	2	AAY22829	Aay22829	SEQ ID NO
35	126	90.6	269	5	ABG68300	Abg68300	Envelope
36	126	90.6	269	5	ABG68307	Abg68307	Envelope
37	126	90.6	269	5	ABG68319	Abg68319	Envelope
38	126	90.6	269	6	ABU57707	Abu57707	Human imm
39	126	90.6	269	6	ABU57726	Abu57726	Human imm
40	126	90.6	269	6	ABU57714	Abu57714	Human imm
41	126	90.6	360	6	ABR57596	Abt57596	HIV gp41
42	126	90.6	850	9	ADK39673	Adk39673	HIV Env p
43	126	90.6	855	9	ADK39674	Adk39674	HIV Env p
44	126	90.6	857	2	AAR12261	Aar12261	HIV-1 btr
45	125	89.9	269	2	AAY22825	Aay22825	SEQ ID NO

ALIGNMENTS

RESULT 1

AY22833	standard; protein; 269 AA.
XX	AY22833;
AC	AY22833;
XX	
DT	19-AUG-1999 (first entry)
XX	
DE	SEQ ID NO. 29 from WO9820036.
XX	
KW	HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
KW	antibody; viral membrane fusion; viral infectivity;
KW	ligand affinity purification; protein A replacement;
KW	immunoglobulin purification; epitope mimic.
XX	
OS	Human immunodeficiency virus.
XX	
PN	WO9820036-A1.
XX	
PD	14-MAY-1998.
XX	
PF	05-NOV-1997; 97WO-US020069.
XX	
PR	06-NOV-1996; 96US-00743698.
XX	
PA	16-JUN-1997; 97US-00876698.
XX	
PI	(GETH) GENENTECH INC.
XX	
PI	Braisted A, Judice JK, McDowell RS, Phelean JC, Starovasmik MA;
XX	Wells JA;
XX	
DR	WPI; 1998-286866/25.
XX	
PT	Production of constrained helical peptide(s) by linking side chains on
PT	termini of octapeptide - derived from human immunodeficiency virus gp41
PT	protein, useful in vaccines for treatment and prevention of infection.
XX	
PS	Claim 11; Page 170; 279pp; English;
XX	

Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and AAY22903 represent consensus sequences of various sections of the gp41 protein). Sequences derived from the peptides are used to produce constrained helical peptides of the invention. The constrained helical peptide is produced by synthesizing an octapeptide in which both terminal amino acids have a side-chain that includes a group able to form an amide

CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 XX
 SQ Sequence 269 AA;
 Query Match 100.0%; Score 139; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 DB 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70
 RESULT 2
 ABG68304
 ID ABG68304 standard; protein; 269 AA.
 XX
 AC ABG68304;
 XX
 XX
 DT 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Envelope protein gp41 from HIV clade B strain #23.
 XX
 KW HIV; glycoprotein; gp41; antigen; helical conformation;
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
 KW viral envelope protein; vaccine; virucide; anti-HIV.
 XX
 OS Human immunodeficiency virus 1; clade B.
 XX
 XX US6271198-B1.
 XX
 XX 07-AUG-2001.
 XX
 XX 05-NOV-1997; 97US-00965056.
 XX
 XX 06-NOV-1996; 96US-00743698.
 XX 16-JUN-1997; 97US-0049787P.
 XX 16-JUN-1997; 97US-00876698.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 XX Wells JA;
 XX WPI; 2002-487624/52.
 XX
 XX New cyclic peptides from human immune deficiency virus gp41, useful for
 XX treatment or prevention of HIV infection, are constrained to have alpha-
 XX helical conformation.
 XX
 XX Disclosure; Col 173-176; 175pp; English.
 XX
 XX The invention relates to cyclic peptides (A) with a constrained helical
 XX conformation, derived from gp41 (glycoprotein 41, a viral envelope
 XX protein) of human immunodeficiency virus (HIV). The cyclic
 XX peptides have formulas given in the specification part of which are
 XX derived from a consensus sequence of gp41 derived from HIV clades A, B,
 XX C, D, E or O. The peptides are used to cause induction of a specific
 XX immune response, resulting in antibodies that prevent virus-induced
 XX membrane fusion. The peptides are used to treat subjects with, or at risk

CC of, HIV infection, either as antifusion/anti-infection agents or,
 CC preferably where associated with a carrier, as an immunogen (including as
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
 CC cases of health care accidents. The peptides can be based on specific HIV
 CC strains, e.g. breakthrough isolates of HIV that have developed during
 CC vaccine trials, so a combination of them should cover a wide range of
 CC protection. The present sequence is gp41 protein from a particular HIV
 CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG--
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 269 AA;
 Query Match 100.0%; Score 139; DB 5; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 DB 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70
 RESULT 3
 ABU57711
 ID ABU57711 standard; protein; 269 AA.
 XX
 AC ABU57711;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Human immunodeficiency virus (HIV) envelope protein gp41 #23.
 XX
 KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
 KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
 KW envelope protein.
 XX
 OS Human immunodeficiency virus.
 XX
 XX US2002151473-A1.
 XX
 XX 17-OCT-2002.
 XX
 XX 15-MAY-2001; 2001US-00854816.
 XX
 XX 06-NOV-1996; 96US-00743698.
 XX 16-JUN-1997; 97US-0049787P.
 XX 16-JUN-1997; 97US-00876698.
 XX 05-NOV-1997; 97US-00965056.
 XX
 XX (BRAI/) BRAISTED A C.
 XX (JUDI/) JUDICE J K.
 XX (MCDO/) MCDOWELL R S.
 XX (PHEL/) PHELAN J C.
 XX (STAR/) STAROVASNIK M A.
 XX (WELL/) WELLS J A.
 XX
 XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 XX Wells JA;
 XX WPI; 2003-182525/18.
 XX
 XX Novel constrained helical peptide compound useful for prophylactically or
 XX therapeutically treating mammal at risk for or infected with human
 XX immunodeficiency virus.
 XX
 XX Disclosure; Fig 16; 180pp; English.
 XX
 XX The invention describes a constrained helical peptide compound (I)
 XX comprising a first constrained helical peptide comprising a sequence of 8
 XX amino acids (a.as) having a first and second terminal residue both
 XX flanking an internal sequence of 6 a.as, where the terminal residues have
 XX a side chain that are linked to each other forming a locking group to

CC form a constrained helical peptide. (I) is useful for preparing
 CC antibodies that prevent viral membrane fusion, as happens, preferably
 CC attached to a carrier, for use as an immunogen to raise antibodies that
 CC have a diagnostic use, as a vaccine for treatment of patients at risk of
 CC or infected with HIV, to create combinatorial constrained helical peptide
 CC libraries that are useful in chemical selection systems, to isolate the
 CC binding determinants from alpha-helical binding domains of known
 CC proteins, for determining whether a binding determinate in an alpha-
 CC helical binding domain of a known protein can serve as a structural model
 CC for the design of peptidomimetics, to replace intact binding proteins or
 CC protein binding domains in the affinity purification of ligands, to mimic
 CC epitopes in proteins to selectively raise polyclonal or monoclonal
 CC antibodies against such individual epitopes for isolating synthetic
 CC antibody clones with a selected binding activity from phage display
 CC combinatorial libraries, to provide conformationally stable variants of
 CC peptides or proteins which exhibit floppy or unstable alpha-helical
 CC secondary structure at one or more sites in unrestrained form under
 CC conditions of interest. This is the amino acid sequence of an HIV
 CC envelope protein gp41, fragments of which are used in the creation of
 CC locked helix peptides

XX Sequence 269 AA;

Query Match 100.0%; Score 139; DB 6; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 |||||
 Db 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 4

AAW44250
 ID AAW44250 standard; protein; 649 AA.

XX AC AAW44250;

DT 17-OCT-2003 (revised)
 DT 26-JUN-1998 (first entry)

XX DE HIV-1 gp160 residues 33-681.

XX KW Vaccine; antibody; antigen; hydrophobic; proteosome; pathogen;
 XX KW immune response; sexually transmitted disease; HIV; infection.

XX OS Human immunodeficiency virus 1.

XX FH Key Location/Qualifiers
 XX FT Region 491..519

XX FT /note= "hydrophobic region"

XX PN W09801558-A2.

XX PD 15-JAN-1998.

XX PF 10-JUL-1997; 97WO-US012253.

XX PR 10-JUL-1996; 96US-0021687P.

XX PA (INTE-) INTELLIVAX INC.

XX PA (JACK-) JACKSON FOUND HENRY M.

XX PA (USSA) US SEC OF ARMY.

XX PI Lowell GH, Vancott TC, Birs DL;

XX DR WPI; 1998-110231/10.

XX FT Vaccine compositions for eliciting neutralising antibodies - comprising
 XX FT antigen containing hydrophobic sequence or having added hydrophobic
 XX FT material, complexed to proteosomes or bio-adhesive nano-emulsions.

XX PS Claim 9; Page 22; 62pp; English.

XX CC The present sequence represents HIV-1 gp160 residues 33-681 (the full
 CC protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine
 CC of the present invention. The vaccine composition is capable of eliciting
 CC neutralising antibodies in a subject to a pathogenic organism which
 CC antibodies are present in vaginal secretions, intestinal secretions, lung
 CC secretions or faeces. The vaccine comprises: (a) an antigen comprising a
 CC protein or peptide having: (i) an endogenous hydrophobic sequence of 3-50
 CC non-polar or uncharged amino acids; (ii) added to the protein or peptide,
 CC an exogenous hydrophobic material comprising a sequence of 3 to 50 non-
 CC polar or uncharged amino acids or a 8-18C fatty acyl group, or (iii) both
 CC (i) and (ii), and (b) complexed with the antigen, a composition
 CC comprising proteosomes, bioadhesive nano-emulsions or both, where the
 CC complexed or coupled protein or peptide maintains a native structure of
 CC antigenic epitopes such that, upon administration to the subject, the
 CC antigen induces neutralising antibodies in one or more of vaginal
 CC secretions, intestinal secretions, lung secretions and faeces, capable of
 CC neutralising the pathogenic organism. The compositions can be used for
 CC inducing an immune response against a pathogenic organism such as a
 CC causative agent of a sexually-transmitted or mucosally-transmitted
 CC disease, e.g. HIV infection. The compositions preserve the antigenic
 CC integrity of the protein or peptide epitopes while at the same time
 CC enhancing their immunogenicity. (Updated on 17-OCT-2003 to standardise OS
 CC field)

XX Sequence 649 AA;

Query Match 100.0%; Score 139; DB 2; Length 649;
 Best Local Similarity 100.0%; Pred. No. 2.3e-10;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 |||||
 Db 491 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 519

RESULT 5

AAW43072

ID AAW43072 standard; peptide; 865 AA.

XX AC AAW43072;

DT 17-OCT-2003 (revised)

DT 11-SEP-1998 (first entry)

XX DE HIV-1 gp120 protein fragment from isolate CDC4.

XX KW gp120 protein; purification; fractionation; ion exchange; chromatography;
 XX KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.

XX OS Human immunodeficiency virus 1.

XX PN US5696238-A.

XX PD 09-DEC-1997.

XX PF 11-MAY-1995; 95US-00439286.

XX PR 20-AUG-1991; 91US-00684963.

XX PR 16-AUG-1993; 93US-00109002.

XX PR 09-MAY-1994; 94US-00240073.

XX PA (CHIR) CHIRON CORP.

XX PI Scandella C, Haigwood NL;

XX DR WPI; 1998-041353/04.

XX PT Purification of HIV gp120 - using chromatographic methods.

XX PS Disclosure; Fig 2A-W; 53pp; English.

XX CC AAW43066-W43080 are fragments of the gp120 protein from different human

CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used
 CC in a novel method for purifying HIV gp120 so as to provide a purified
 CC gp120 glycoprotein having protein/protein binding properties
 CC substantially identical to natural viral HIV gp120. The method involves
 CC fractionating a crude gp120 preparation containing full-length,
 CC glycosylated gp120 using ion exchange chromatography so as to provide a
 CC first collection of fractions. A fraction from the first collection is
 CC selected that exhibits specific binding affinity for CD4 peptide, thereby
 CC producing a first fractionated material. The first fractionated material
 CC is fractionated by hydrophobic interaction chromatography so as to
 CC provide a second collection of fractions from which a second collection
 CC is selected that exhibits specific binding affinity for CD4 peptide. This
 CC second fraction is fractionated by size exclusion chromatography so as to
 CC provide a third collection of fractions exhibiting specific binding
 CC affinity for CD4 peptide, thereby providing the purified gp120. The
 CC purified gp120 can be used for antibody production and in vaccines.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX
 SQ Sequence 865 AA;

Query Match 100.0%; Score 139; DB 2; Length 865;
 Best Local Similarity 100.0%; Pred. No. 3.1e-10; Indels 0; Gaps 0;
 Matches 29; Conservative 0; Mismatches 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 521 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 549
 |||||

RESULT 6
 ABP73114
 ID ABP73114 standard; protein; 669 AA.

AC ABP73114;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant gp140.

DE Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g12;
 KW gp140.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43017.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 17; Page 91-94; 127pp; French.

XX The present sequence represents a truncated variant, designated gp140, of
 CC the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
 CC glycoprotein mutant g12 (see ACC43015 and ABP73112). The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides

CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
 Best Local Similarity 93.1%; Pred. No. 2.9e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527
 |||||

RESULT 7

ABP73117

ID ABP73117 standard; protein; 669 AA.

XX AC ABP73117;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant gp140.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112;
 KW gp140.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43020.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 20; Page 99-102; 127pp; French.

XX The present sequence represents a truncated variant, designated gp140, of
 CC the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
 CC glycoprotein mutant g112 (see ACC43018 and ABP73115). The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection

XX Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
 Best Local Similarity 93.1%; Pred. No. 2.9e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527
 |||||

RESULT 8

ABP73122

ID ABP73122 standard; protein; 669 AA.

```

XX AC ABP73122;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of a HIV-1 envelope protein mutant.
XX KW Envelope glycoprotein; HIV-1; vaccine; HIV infection.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN WO2003020755-A1.
XX FD 13-MAR-2003.
XX PF 06-SEP-2002; 2002WO-FR003039.
XX PR 06-SEP-2001; 2001FR-00011699.
XX FA (INMR ) BIOMERIEUX SA.
XX PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX DR WPI; 2003-278759/27.
XX DR N-PSDB; ACC43025.
XX PT New mutated env gene of human immune deficiency virus, useful for genetic
XX PT vaccination, also derived polypeptides having asparagine replaced by
XX PT glutamine.
XX PS Claim 12; Page 108-110; 127pp; French.
XX CC The present sequence represents a truncated variant, designated gp140, of
XX CC the human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
XX CC glycoprotein mutant g14 (see ACC43021 and ABP731118). The specification
XX CC describes mutated HIV-1 envelope glycoproteins that have at least two
XX CC mutations at glycosylation sites, conserved among primary isolates, each
XX CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
XX CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
XX CC are used in vaccines for prevention and treatment of HIV infection
XX SQ Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
Best Local Similarity 93.1%; Pred. No. 2.9e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAGSTMGAAASLALTV 527
|||||
RESULT 10
ABP73115
ID ABP73115 standard; protein; 844 AA.
XX AC ABP73115;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of HIV-1 envelope protein mutant g112.
XX KW Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN WO2003020755-A1.
XX PD 13-MAR-2003.
XX PF 06-SEP-2002; 2002WO-FR003039.
XX PR 06-SEP-2001; 2001FR-00011699.
XX FA (INMR ) BIOMERIEUX SA.
XX PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX DR WPI; 2003-278759/27.
XX DR N-PSDB; ACC43018.
XX PT New mutated env gene of human immune deficiency virus, useful for genetic
XX PT vaccination, also derived polypeptides having asparagine replaced by
XX PT glutamine.
XX PS Claim 20; Page 94-97; 127pp; French.
XX CC The present sequence represents the Human immunodeficiency virus type 1

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CC (HIV-1) isolate 133 envelope glycoprotein mutant g112. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 527

RESULT 11
 ABP73112
 ID ABP73112 standard; protein; 844 AA.

AC ABP73112;
 XX
 DT 17-JUN-2003 (first entry)

XX Amino acid sequence of HIV-1 envelope protein mutant g12.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g12.

OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 PN WO2003020755-A1.

XX
 PD 13-MAR-2003.

PF 06-SEP-2002; 2002WO-FR003039.

PR 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

DR WPI; 2003-278759/27.

DR N-PSDB; ACC43015.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 17; Page 85-89; 127pp; French.

XX The present sequence represents the Human immunodeficiency virus type 1
 CC (HIV-1) isolate 133 envelope glycoprotein mutant g12. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 527

RESULT 12
 ABP73118

ID ABP73118 standard; protein; 844 AA.

XX
 AC ABP73118;

XX
 DT 17-JUN-2003 (first entry)

XX Amino acid sequence of HIV-1 envelope protein mutant g14.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g14.

OS Synthetic.

OS Human immunodeficiency virus 1.

XX
 PN WO2003020755-A1.

XX
 PD 13-MAR-2003.

PF 06-SEP-2002; 2002WO-FR003039.

PR 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

DR WPI; 2003-278759/27.

DR N-PSDB; ACC43021.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 12; Page 102-103; 127pp; French.

XX The present sequence represents the Human immunodeficiency virus type 1
 CC (HIV-1) isolate 133 envelope glycoprotein mutant g14. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;

Best Local Similarity 93.1%; Pred. No. 3.7e-09;

Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 29

|||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTV 527

RESULT 13
 ABP73121

ID ABP73121 standard; protein; 844 AA.

XX
 AC ABP73121;

XX
 DT 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant.

XX Envelope glycoprotein; HIV-1; vaccine; HIV infection.

OS Synthetic.

OS Human immunodeficiency virus 1.

XX
 PN WO2003020755-A1.

XX
 PD 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.
 XX
 XX 06-SEP-2001; 2001FR-00011699.
 PR
 XX (INNR) BIOMERIEUX SA.
 XX
 XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
 PI
 XX WPI; 2003-278759/27.
 XX
 XX N-PSDB; ACC43024.
 DR
 XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.
 XX
 XX Disclosure; Page 113-116; 127pp; French.
 PS
 XX The present sequence represents a Human immunodeficiency virus type 1
 CC (HIV-1) envelope glycoprotein mutant. The specification describes mutated
 CC HIV-1 envelope glycoproteins that have at least two mutations at
 CC glycosylation sites, conserved among primary isolates, each consisting of
 CC replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated
 CC envelope glycoprotein polynucleotides and polypeptides are used in
 CC vaccines for prevention and treatment of HIV infection
 XX
 XX Sequence 844 AA;
 SQ

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
 |||||
 Db 499 AVGMGLAMFLGFLGAGSTMGATSMALTV 527

RESULT 14
 ABP73111
 ID ABP73111 standard; protein; 844 AA.
 XX
 AC ABP73111;
 XX
 DT 23-OCT-2003 (revised)
 DT 17-JUN-2003 (first entry)
 XX
 XX Amino acid sequence of the envelope protein of HIV-1 isolate 133.
 XX
 XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; gene.
 KW
 XX Human immunodeficiency virus 1.
 XX
 XX WO2003020755-A1.
 PN
 XX
 XX 13-MAR-2003.
 FD
 XX
 XX 06-SEP-2002; 2002WO-FR003039.
 XX
 XX 06-SEP-2001; 2001FR-00011699.
 PR
 XX (INNR) BIOMERIEUX SA.
 PA
 XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
 PI
 XX WPI; 2003-278759/27.
 XX
 XX N-PSDB; ACC43014.
 DR
 XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.
 XX
 XX Disclosure; Page 82-85; 127pp; French.
 PS
 XX

CC The present sequence represents an envelope glycoprotein of Human
 CC immunodeficiency virus type 1 (HIV-1) isolate 133. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection.
 CC (Updated on 23-OCT-2003 to standardise OS field)
 XX
 XX Sequence 844 AA;
 SQ

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
 |||||
 Db 499 AVGMGLAMFLGFLGAGSTMGATSMALTV 527

RESULT 15
 ADX39690
 ID ADX39690 standard; protein; 791 AA.
 XX
 AC ADX39690;
 XX
 DT 21-APR-2005 (first entry)
 DT
 XX HIV Env protein #99.
 DE
 XX Immune stimulation; Env.
 KW
 XX Human immunodeficiency virus.
 OS
 XX WO2005012502-A2.
 PN
 XX 10-FEB-2005.
 PD
 XX
 XX 29-MAR-2004; 2004WO-US009510.
 PF
 XX 28-MAR-2003; 2003US-0458026P.
 PR
 XX (EPIM-) EPIMUNE INC.
 XX
 XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 PI
 XX WPI; 2005-132661/14.
 DR
 XX Identifying a candidate peptide epitope, which induces a HLA class I CTL
 PT response comprises identifying variants of a peptide epitope 8-11 amino
 PT acids in length comprising primary anchor residues of the same HLA class
 PT I binding motif.
 XX
 XX Disclosure; Page 180-231; 458pp; English.
 PS
 XX The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Env protein used in the scope of the invention.
 XX
 XX Sequence 791 AA;
 SQ

Query Match 93.5%; Score 130; DB 9; Length 791;
 Best Local Similarity 93.1%; Pred. No. 4.7e-09;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
 |||||
 Db 514 AVGMGLAMFLGFLGAGSTMGATSMALTV 542

Search completed: March 7, 2006, 17:45:24
Job time : 12.7198 secs

C;superfamily: type E r

Db 511 AVGAIGAMFLGFLGAAGSTMGAASLTIV 539

RESULT 10

S60689
env protein - human immunodeficiency virus type 1 (isolate 2051) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60689
R/Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994
A/Title: Molecular epidemiology of HIV-1 in Madrid.
A/Reference number: S60687; MUID:94249284; PMID:7545926
A/Accession: S60689
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-69 <ROJ>
A/Cross-references: UNIPROT:Q76152; UNIPARC:UPI000010A870; EMBL:Z29691; NID:9808979; PID:
C/Superfamily: type E retrovirus env polyprotein

Query Match 83.5%; Score 116; DB 2; Length 69;
Best Local Similarity 79.3%; Pred. No. 1.7e-08;
Matches 23; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAAGSTMGAATLV 29
||||:|||||
Db 8 AVGMIGAVFLGFLGAAGSTMGAASLTIV 36
||||:|||||

RESULT 11

S60691
env protein - human immunodeficiency virus type 1 (isolate D5/-2) (fragment)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60691
R/Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994
A/Title: Molecular epidemiology of HIV-1 in Madrid.
A/Reference number: S60687; MUID:94249284; PMID:7545926
A/Accession: S60691
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-69 <ROJ>
A/Cross-references: UNIPROT:Q76154; UNIPARC:UPI0000107C1C; EMBL:Z29919; NID:9808983; PID:
C/Superfamily: type E retrovirus env polyprotein

Query Match 82.0%; Score 114; DB 2; Length 69;
Best Local Similarity 75.9%; Pred. No. 3e-08;
Matches 22; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAAGSTMGAATLV 29
||||:|||||
Db 8 AVGVIGALFLGFLGAAGSTMGAASLTIV 36
||||:|||||

RESULT 12

S60525
envelope glycoprotein gp41 - human immunodeficiency virus type 1 (isolate CI-13-3 and iso
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate CI-13-3; isolate CI-13-4
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S60525; S60527
R/Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A/Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A/Reference number: S60521; MUID:94280700; PMID:8011235
A/Accession: S60525
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-294 <JAN>
A/Cross-references: UNIPROT:Q76169; UNIPROT:Q76170; UNIPARC:UPI0000102742; EMBL:X72028; I
A/Experimental source: isolate CI-13-3
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993

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OM protein - protein search, using sw_model

Run on: March 7, 2006, 17:40:55 ; Search time 13.3024 Seconds
(without alignments)
1538.097 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551
Perfect score: 139
Sequence: 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	868	1 ENV HVIC4	P05879 human immun
2	132	95.0	877	2 Q6IUG0	Q6IUG0 human immun
3	132	95.0	877	2 Q6IUG1	Q6IUG1 human immun
4	132	95.0	877	2 Q6IUG2	Q6IUG2 human immun
5	131	94.2	799	2 Q6QLA1	Q6QLA1 human immun
6	131	94.2	814	2 Q6QLK5	Q6QLK5 human immun
7	131	94.2	844	2 Q6QLK7	Q6QLK7 human immun
8	131	94.2	844	2 Q6QLK8	Q6QLK8 human immun
9	131	94.2	844	2 Q6QLK9	Q6QLK9 human immun
10	131	94.2	844	2 Q6QLK0	Q6QLK0 human immun
11	131	94.2	844	2 Q6QLJ4	Q6QLJ4 human immun
12	131	94.2	859	2 Q6QLJ5	Q6QLJ5 human immun
13	131	94.2	859	2 Q6QLJ6	Q6QLJ6 human immun
14	131	94.2	859	2 Q6QLJ7	Q6QLJ7 human immun
15	131	94.2	859	2 Q6QLJ8	Q6QLJ8 human immun
16	131	94.2	859	2 Q6QLJ9	Q6QLJ9 human immun
17	131	94.2	859	2 Q6QLK0	Q6QLK0 human immun
18	131	94.2	859	2 Q6QLK1	Q6QLK1 human immun
19	131	94.2	859	2 Q6QLK2	Q6QLK2 human immun
20	131	94.2	859	2 Q6QLK3	Q6QLK3 human immun
21	131	94.2	859	2 Q6QLK4	Q6QLK4 human immun
22	131	94.2	859	2 Q6QLK5	Q6QLK5 human immun
23	131	94.2	859	2 Q6QLK6	Q6QLK6 human immun
24	131	94.2	868	2 Q6QLK3	Q6QLK3 human immun
25	130	93.5	858	2 Q7SUT2	Q7SUT2 human immun
26	130	93.5	859	2 P87924	P87924 human immun
27	130	93.5	859	2 Q7SUT4	Q7SUT4 human immun
28	130	93.5	859	2 Q7SUT6	Q7SUT6 human immun
29	130	93.5	859	2 Q7SUT7	Q7SUT7 human immun
30	130	93.5	859	2 Q7SUT8	Q7SUT8 human immun
31	130	93.5	859	2 Q7SUT9	Q7SUT9 human immun

32	130	93.5	865	2 Q7SUT5	Q7SUT5 human immun
33	129	92.8	855	1 ENV HVIC4	ENV HVIC4
34	128	92.1	797	2 Q03808	Q03808 human immun
35	128	92.1	797	2 Q03810	Q03810 human immun
36	128	92.1	799	2 Q03807	Q03807 human immun
37	128	92.1	801	2 Q03809	Q03809 human immun
38	128	92.1	852	2 Q69992	Q69992 human immun
39	128	92.1	857	2 Q7ZJ87	Q7ZJ87 human immun
40	128	92.1	857	2 Q9DQ26	Q9DQ26 human immun
41	128	92.1	858	2 Q9PY30	Q9PY30 human immun
42	128	92.1	861	2 Q7SUV9	Q7SUV9 human immun
43	127	91.4	387	2 Q6JE18	Q6JE18 human immun
44	127	91.4	844	2 Q6QLL2	Q6QLL2 human immun
45	127	91.4	848	2 Q6HIR8	Q6HIR8 human immun

ALIGNMENTS

RESULT 1

ENV HVIC4 STANDARD; PRT; 868 AA.
AC P05879;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE Name=ENV;
GN Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11687;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Desai S.M., Kalyanaram V.S., Casey J.M., Srinivasan A., Andersen P.R., Devare S.G.;
RA "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
RL [2]
RN PROTEIN SEQUENCE OF 34-43.
RP MEDLINE=90253924; PubMed=2187500;
RA Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P., DeVico A.L., Copeland T., Oroszian S., Gallo R.C., Sarnagadharan M.G.;
RA "Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1";
RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL: M13137; AAA44311.1; -; Genomic_RNA.
DR PIR: C25523; VCLJH4.
DR HSP: P19549; IMEQ.
DR SMR: P05879; 84-128, 87-212, 206-503, 552-638.
DR HIV: M13137; ENV5CDC45.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Capsid protein; Direct protein sequencing; Glycoprotein; Polyprotein; Signal; Structural protein; Transmembrane.
KW AIDS; Capsid protein; Direct protein sequencing; Glycoprotein; Polyprotein; Signal; Structural protein; Transmembrane.
FT SIGNAL 1 33
FT CHAIN 34 522 Exterior membrane glycoprotein.
FT CHAIN 523 868 Transmembrane glycoprotein.
FT CARBOHYD 89 89 N-linked (GlcNAc...) (potential).
FT CARBOHYD 131 131 N-linked (GlcNAc...) (potential).

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FT CARBOHYD 138 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 139 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 142 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 162 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 166 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 195 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 198 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 208 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 245 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 252 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 273 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 287 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 300 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 306 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 312 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 342 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 349 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 365 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 371 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 395 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 405 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 409 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 459 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 473 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 623 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 628 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 637 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 649 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 828 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 55 By similarity.
FT DISULFID 120 By similarity.
FT DISULFID 127 By similarity.
FT DISULFID 132 By similarity.
FT DISULFID 229 By similarity.
FT DISULFID 239 By similarity.
FT DISULFID 307 By similarity.
FT DISULFID 387 By similarity.
FT DISULFID 394 By similarity.
SQ SEQUENCE 868 AA; 98699 MW; A11527FC52A6F0C8 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 28-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
DB 523 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 551

RESULT 2
Q6IUG0_9HIV1
ID Q6IUG0_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gorby P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R.,
RA Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H.,
RA Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
RA Gabuzda D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY624307; AAT4420.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; P04578; 80-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99339 MW; 81FF9C9641E832C CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
DB 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 4
Q6IUG2_9HIV1
ID Q6IUG2_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
```

```
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99229 MW; D5F0E3B9A831EE3F CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
DB 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 3
Q6IUG1_9HIV1
ID Q6IUG1_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gorby P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R.,
RA Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H.,
RA Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
RA Gabuzda D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY624306; AAT4419.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; P04578; 80-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99339 MW; 81FF9C9641E832C CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
DB 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 4
Q6IUG2_9HIV1
ID Q6IUG2_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RN NUCLEOTIDE SEQUENCE.
 RA Gory P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R.,
 RA Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H.,
 RA Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
 RA Gabuzda D.,
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY624304; AAT44417.1; -; Genomic_DNA.
 DR HSP; P04578; IK33.
 DR SMR; Q6IUG2; 80-134, 561-647.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR GO; GO:0005328; Env GP41.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Envelope protein; Transmembrane.
 KW AIDS; Envelope protein; Transmembrane.
 SQ SEQUENCE 877 AA; 99362 MW; 55212AEE17198A77 CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
 Best Local Similarity 93.1%; Pred. No. 1.6e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
 |||||
 Db 532 AVGMGLGAMFLGFLGAGSTMGATSMALTV 560

RESULT 5
 Q6QLL1_9HIV1
 ID Q6QLL1_9HIV1 PRELIMINARY; PRT; 799 AA.
 AC Q6QLL1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=133;
 RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.,
 RA "Evolutionary Dynamics of the Glycan Shield of the Human
 RT Immunodeficiency Virus Envelope during Natural Infection and
 RT Implications for Exposure of the 2G12 Epitope."
 RL J. Virol. 78:12625-12637(2004).
 DR EMBL; AY535428; AAS58771.1; -; Genomic_RNA.
 DR SMR; Q6QLL1; 140-479, 528-614.
 DR GO; GO:0042025; C: host cell nucleus; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR GO; GO:0003700; F: transcription factor activity; IEA.
 DR GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00424; REV; 1.
 KW Envelope protein.
 SQ SEQUENCE 799 AA; 89998 MW; A42EF332C626DF65 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 799;
 Best Local Similarity 93.1%; Pred. No. 2e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
 |||||

Db 499 AVGMGLGAMFLGFLGAGSTMGATSMALTV 527

RESULT 6
 Q6QLK5_9HIV1
 ID Q6QLK5_9HIV1 PRELIMINARY; PRT; 814 AA.
 AC Q6QLK5;
 DT 05-JUN-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=133;
 RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.,
 RA "Evolutionary Dynamics of the Glycan Shield of the Human
 RT Immunodeficiency Virus Envelope during Natural Infection and
 RT Implications for Exposure of the 2G12 Epitope."
 RL J. Virol. 78:12625-12637(2004).
 DR EMBL; AY535434; AAS58777.1; -; Genomic_RNA.
 DR SMR; Q6QLK5; 200-494, 543-629.
 DR GO; GO:0042025; C: host cell nucleus; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR GO; GO:0003700; F: transcription factor activity; IEA.
 DR GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00424; REV; 1.
 KW Envelope protein.
 SQ SEQUENCE 814 AA; 91785 MW; 8AAB45F6CA6953A1 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 814;
 Best Local Similarity 93.1%; Pred. No. 2e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
 |||||
 Db 514 AVGMGLGAMFLGFLGAGSTMGATSMALTV 542

RESULT 7
 O56561_9HIV1
 ID O56561_9HIV1 PRELIMINARY; PRT; 844 AA.
 AC O56561;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99372987; PubMed=10445815; DOI=10.1089/089922299310548;
 RA Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron F.,
 RA Verrier B.,
 RA "Comparison of complete env gene sequences from individuals with
 RT symptomatic primary HIV type 1 infection.";
 RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL; AF041126; AAC02517.1; -; Genomic_DNA.
 DR HSP; P04578; IK34.


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Db 499 AVGMGLAMFLGFLGAAGSTMGAASLALTV 527

RESULT 11
ID Q6QLJ4_9HIV1 PRELIMINARY; PRT; 844 AA.
AC Q6QLJ4_9HIV1 PRELIMINARY; PRT; 844 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY354429; AAS58772.1; -; Genomic_RNA.
DR SMR; Q6QLJ4; 140-479, 528-614.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 844 AA; 95807 MW; 17A31D1BD9CF0ADC CRC64;

Query Match 94.2%; Score 131; DB 2; Length 844;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 499 AVGMGLAMFLGFLGAAGSTMGAASLALTV 527

RESULT 12
ID Q6QLJ4_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ4_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY354446; AAS58789.1; -; Genomic_RNA.
DR SMR; Q6QLJ4; 200-494, 543-629.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97398 MW; 8378D387EA019CD2 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 514 AVGMGLAMFLGFLGAAGSTMGAASLALTV 542

RESULT 13
ID Q6QLJ5_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ5_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY353445; AAS58788.1; -; Genomic_RNA.
DR SMR; Q6QLJ5; 200-494, 543-629.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97398 MW; 8378D387EA019CD2 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 514 AVGMGLAMFLGFLGAAGSTMGAASLALTV 542

RESULT 14
ID Q6QLJ6_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ6_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
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Job time : 14.3024 secs

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78:12625-12637(2004).
DR ENBL; AY535444; AAS58787.1; -; Genomic_RNA.
DR SMR; Q6QLJ6; 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97581 MW; CDFE3D498277012B CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
DB 514 AVGMGLGAMFLGFLGAGSTMGASLALTV 542

RESULT 15
Q6QLJ7_9HIV1
ID Q6QLJ7_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78:12625-12637(2004).
DR ENBL; AY535442; AAS58785.1; -; Genomic_RNA.
DR SMR; Q6QLJ7; 200-494, 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97483 MW; 5B54B76D5F4245A8 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
DB 514 AVGMGLGAMFLGFLGAGSTMGASLALTV 542

Search completed: March 7, 2006, 17:50:38
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:03 ; Search time 3.03687 Seconds
(without alignments)
789.495 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551
Perfect score: 139
Sequence: 1 AVGMGLGAMFLGFLGAGSTGATSMALTV 29

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	129	92.8	269	2	US-08-965-056-27
3	128	92.1	269	2	US-08-965-056-47
4	127	91.4	269	2	US-08-965-056-12
5	127	91.4	855	2	US-07-956-483-14
6	127	91.4	887	2	US-08-472-240A-5
7	126	90.6	269	2	US-08-965-056-25
8	126	90.6	269	2	US-08-965-056-32
9	126	90.6	269	2	US-08-965-056-44
10	125	89.9	269	2	US-08-965-056-21
11	124	89.2	79	2	US-08-965-056-58
12	124	89.2	269	2	US-08-965-056-36
13	124	89.2	269	2	US-08-965-056-43
14	124	89.2	269	2	US-08-965-056-46
15	123	88.5	269	2	US-08-965-056-31
16	123	88.5	269	2	US-08-965-056-42
17	122	87.8	269	2	US-08-965-056-6
18	122	87.8	269	2	US-08-965-056-23
19	122	87.8	269	2	US-08-965-056-24
20	121	87.1	105	2	US-08-965-056-52
21	121	87.1	105	2	US-08-965-056-54
22	120	86.3	40	2	US-08-948-782-3
23	120	86.3	40	2	US-09-482-612-3
24	120	86.3	40	2	US-09-677-554-3
25	120	86.3	269	2	US-08-965-056-28
26	120	86.3	269	2	US-08-965-056-30
27	120	86.3	269	2	US-08-965-056-45

28	120	86.3	610	2	US-09-257-490-12	Sequence 12, Appl
29	120	86.3	855	2	US-07-956-483-15	Sequence 15, Appl
30	120	86.3	887	2	US-08-472-240A-6	Sequence 6, Appl
31	118	84.9	79	2	US-08-965-056-60	Sequence 60, Appl
32	118	84.9	269	2	US-08-965-056-22	Sequence 22, Appl
33	118	84.9	880	1	US-08-788-815-7	Sequence 7, Appl
34	118	84.9	880	2	US-09-157-963-7	Sequence 7, Appl
35	118	84.9	880	2	US-09-568-105-7	Sequence 7, Appl
36	118	84.9	906	2	US-08-472-240A-3	Sequence 3, Appl
37	117	84.2	79	2	US-08-965-056-34	Sequence 59, Appl
38	117	84.2	269	2	US-08-965-056-33	Sequence 33, Appl
39	116	83.5	269	2	US-08-965-056-67	Sequence 67, Appl
40	116	83.5	270	2	US-08-965-056-13	Sequence 13, Appl
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44	114	82.0	269	2	US-08-965-056-48	Sequence 76, Appl
45	114	82.0	269	2	US-08-965-056-76	

ALIGNMENTS

RESULT 1
US-08-965-056-29 ; Sequence 29, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasinik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-965-056-29

Query Match 100.0%; Score 139; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVGMGLGAMFLGFLGAGSTGATSMALTV 29
|||||

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 2

US-08-965-056-27
; Sequence 27, Application US/08965056
; Patent No. 6271198

; GENERAL INFORMATION:

; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasknik
; APPLICANT: James A. Wells

; TITLE OF INVENTION: Constrained Helical Peptides and Methods of

; TITLE OF INVENTION: Making Same

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/965,056

; FILING DATE: 05-No. 6271198-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1005R2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-965-056-27

Query Match 92.8%; Score 129; DB 2; Length 267;

Best Local Similarity 93.1%; Pred. No. 7.5e-11;

Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGATSMALTV 29

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 3

US-08-965-056-47

; Sequence 47, Application US/08965056

; Patent No. 6271198

; GENERAL INFORMATION:

; APPLICANT: Andrew C. Braisted

; APPLICANT: J. Kevin Judice

; APPLICANT: Robert S. McDowell

; APPLICANT: J. Christopher Phelan

; APPLICANT: Melissa A. Starovasknik

; APPLICANT: James A. Wells

; TITLE OF INVENTION: Constrained Helical Peptides and Methods of

; TITLE OF INVENTION: Making Same

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/965,056

; FILING DATE: 05-No. 6271198-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1005R2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 269 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-965-056-47

Query Match

Best Local Similarity 92.1%; Score 128; DB 2; Length 269;

Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGATSMALTV 29

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 4

US-08-965-056-12

; Sequence 12, Application US/08965056

; Patent No. 6271198

; GENERAL INFORMATION:

; APPLICANT: Andrew C. Braisted

; APPLICANT: J. Kevin Judice

; APPLICANT: Robert S. McDowell

; APPLICANT: J. Christopher Phelan

; APPLICANT: Melissa A. Starovasknik

; APPLICANT: James A. Wells

; TITLE OF INVENTION: Constrained Helical Peptides and Methods of

; TITLE OF INVENTION: Making Same

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/965,056

; FILING DATE: 05-No. 6271198-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1005R2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-965-056-12

Query Match 91.4%; Score 127; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AVGMGLAMFLGLGAGSTMGTATMLTV 29
||| : ||||| ||||| ||||| ||||| |||||
Db 42 AVGTIGAMFLGLGAGSTMGTATMLTV 70

RESULT 5

US-07-956-483-14
Sequence 14, Application US/07956483
Patent No. 6261799

GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: GP160 VARIANT
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/19742
FILING DATE: 12-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392

FILING DATE: 02-MAY-1991

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113

REFERENCE/DOCKET NUMBER: 017753-005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 855 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-956-483-14

Query Match 91.4%; Score 127; DB 2; Length 855;
Best Local Similarity 89.7%; Pred. No. 5.5e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AVGMGLAMFLGLGAGSTMGTATMLTV 29
||| : ||||| ||||| ||||| ||||| |||||
Db 511 AVGTIGAMFLGLGAGSTMGTATMLTV 539

RESULT 6

US-08-472-240A-5

Sequence 5, Application US/08472240A
Patent No. 6284248

GENERAL INFORMATION:

APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: GP160 VARIANT
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,240A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/956,483

FILING DATE: 31-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 017753-055

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 887 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Protein

LOCATION: 1..854

US-08-472-240A-5

Query Match 91.4%; Score 127; DB 2; Length 887;

Best Local Similarity 89.7%; Pred. No. 5.8e-10;

Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AVGMGLAMFLGLGAGSTMGTATMLTV 29
||| : ||||| ||||| ||||| ||||| |||||

Db 542 AVGTIGAMFLGLGAGSTMGTATMLTV 570

RESULT 7

US-08-965-056-25

Sequence 25, Application US/08965056
Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judice

APPLICANT: Robert S. McDowell

APPLICANT: J. Christopher Phelan

APPLICANT: Melissa A. Starovasnik

APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

TITLE OF INVENTION: Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

```

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-25
;
;
Query Match 90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTV 70

RESULT 8
US-08-965-056-32
; Sequence 32, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovashnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; ADDRESS: Genentech, Inc.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-32
;
;
Query Match 90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTV 70

RESULT 9
US-08-965-056-44
; Sequence 44, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovashnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; ADDRESS: Genentech, Inc.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-44
;
;
Query Match 90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 10
US-08-965-056-21
; Sequence 21, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovashnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; ADDRESS: Genentech, Inc.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-21
;
;
Query Match 90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTV 70
```


Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAAASVALTV 70

RESULT 13
US-08-965-056-43
; Sequence 43, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasinik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-46

Query Match 89.2%; Score 124; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAAASVALTV 70

RESULT 14
US-08-965-056-46
; Sequence 46, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasinik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of

; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-46

Query Match 89.2%; Score 124; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAAASVALTV 70

RESULT 15
US-08-965-056-31
; Sequence 31, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasinik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.

; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-31

Query Match 88.5%; Score 123; DB 2; Length 269;
Best Local Similarity 86.2%; Pred No. 5.5e-10;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGNLGMFLGFLGAGSTMGATSMALTV 29
|||:|||||
Db 42 AVGIIGAMFLGFLGAGSTMGARSMTLTV 70
|||:|||||

Search completed: March 7, 2006, 17:52:52
Job time : 4.03687 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 9.4528 Seconds
(without alignments)
1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLGMFLGFLGAGSTWGTSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	269	3	US-09-854-816-29
2	139	100.0	868	3	US-09-938-406-1
3	131	94.2	669	5	US-10-487-094-14
4	131	94.2	669	5	US-10-487-094-17
5	131	94.2	669	5	US-10-487-094-20
6	131	94.2	669	5	US-10-487-094-25
7	131	94.2	844	5	US-10-487-094-11
8	131	94.2	844	5	US-10-487-094-12
9	131	94.2	844	5	US-10-487-094-15
10	131	94.2	844	5	US-10-487-094-18
11	131	94.2	844	5	US-10-487-094-24
12	130	93.5	883	4	US-10-441-926-2
13	130	93.5	883	4	US-10-441-949-2
14	130	93.5	883	5	US-10-780-507-2
15	130	93.5	883	5	US-10-780-507-121
16	129	92.8	267	3	US-09-854-816-27
17	128	92.1	269	3	US-09-854-816-47
18	127	91.4	269	3	US-09-854-816-12
19	126	90.6	269	3	US-09-854-816-25
20	126	90.6	269	3	US-09-854-816-32
21	126	90.6	269	3	US-09-854-816-44
22	126	90.6	360	4	US-10-214-670-60
23	125	89.9	269	3	US-09-854-816-21
24	124	89.2	79	3	US-09-854-816-58
25	124	89.2	269	3	US-09-854-816-36
26	124	89.2	269	3	US-09-854-816-43
27	124	89.2	269	3	US-09-854-816-46

28	124	89.2	862	5	US-10-780-507-50	Sequence 50, Appl
29	123	88.5	269	3	US-09-854-816-31	Sequence 31, Appl
30	123	88.5	269	3	US-09-854-816-42	Sequence 42, Appl
31	122	87.8	269	3	US-09-854-816-6	Sequence 6, Appl
32	122	87.8	269	3	US-09-854-816-23	Sequence 23, Appl
33	122	87.8	269	3	US-09-854-816-24	Sequence 24, Appl
34	121	87.1	105	3	US-09-854-816-52	Sequence 52, Appl
35	121	87.1	105	3	US-09-854-816-54	Sequence 54, Appl
36	121	87.1	848	5	US-10-844-858-1	Sequence 1, Appl
37	120	86.3	269	3	US-09-854-816-28	Sequence 28, Appl
38	120	86.3	269	3	US-09-854-816-30	Sequence 30, Appl
39	120	86.3	269	3	US-09-854-816-45	Sequence 45, Appl
40	120	86.3	862	5	US-10-780-507-51	Sequence 51, Appl
41	118	84.9	79	3	US-09-854-816-60	Sequence 60, Appl
42	118	84.9	269	3	US-09-854-816-22	Sequence 22, Appl
43	118	84.9	852	4	US-10-093-953A-29	Sequence 29, Appl
44	117	84.2	79	3	US-09-854-816-59	Sequence 59, Appl
45	117	84.2	269	3	US-09-854-816-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-854-816-29
; Sequence 29, Application US/09854816
; Patent NO. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasiluk
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-854-816-29
Query Match 100.0%; Score 139; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
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Db 42 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 70

RESULT 2

US-09-938-406-1
; Sequence 1, Application US/09938406
; Patent No. US20020155120A1
; GENERAL INFORMATION:
; APPLICANT: Lowell, George
; APPLICANT: Vancott, Thomas
; APPLICANT: Birk, Deborah
; TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
; FILE REFERENCE: 40646-20002.10
; CURRENT APPLICATION NUMBER: US/09/938,406
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/214,701
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/US 97/12253
; PRIOR FILING DATE: 1997-07-10
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Virus HIV-1
US-09-938-406-1

Query Match 100.0%; Score 139; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
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Db 523 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 551

RESULT 3

US-10-487-094-14
; Sequence 14, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g12
US-10-487-094-14

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527

RESULT 4

US-10-487-094-17
; Sequence 17, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g112
US-10-487-094-17

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527

RESULT 5

US-10-487-094-20
; Sequence 20, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g14
US-10-487-094-20

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527

RESULT 6

US-10-487-094-25
; Sequence 25, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic

```
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g22
US-10-487-094-25

Query Match          94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 527

RESULT 7
US-10-487-094-11
; Sequence 11, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 133
US-10-487-094-11

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 527

RESULT 8
US-10-487-094-12
; Sequence 12, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g12
US-10-487-094-12

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 527

RESULT 9
US-10-487-094-15
; Sequence 15, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g112
US-10-487-094-15

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 527

RESULT 10
US-10-487-094-18
; Sequence 18, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g14
US-10-487-094-18

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
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Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTGATSMALTV 29
Db 499 AVGMGLAMFLGLGAAGSTMGTGASMLTIV 527

RESULT 11
US-10-487-094-24
; Sequence 24, Application US/10487094
; Publication No. US20050063320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g22
US-10-487-094-24

Query Match 94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTGATSMALTV 29
Db 499 AVGMGLAMFLGLGAAGSTMGTGASMLTIV 527

RESULT 12
US-10-441-926-2
; Sequence 2, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-011001
; CURRENT APPLICATION NUMBER: US/10/441,926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide
US-10-441-926-2

Query Match 93.5%; Score 130; DB 4; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLAMFLGLGAAGSTMGTGASMTLTV 566

RESULT 13
US-10-441-949-2
; Sequence 2, Application US/10441949
; Publication No. US20040116684A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-012001
; CURRENT APPLICATION NUMBER: US/10/441,949
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide
US-10-441-949-2

Query Match 93.5%; Score 130; DB 4; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLAMFLGLGAAGSTMGTGASMTLTV 566

RESULT 14
US-10-780-507-2
; Sequence 2, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence
US-10-780-507-2

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AVGMGLGAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLGAMFLGLGAAGSTMGTGASMTLTV 566

RESULT 15

US-10-780-507-121
; Sequence 121, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
US-10-780-507-121

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLGAMFLGLGAAGSTMGTGASMTLTV 566

Search completed: March 7, 2006, 17:56:39
Job time : 10.4528 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:53:05 ; Search time 1.11209 Seconds
(without alignments)
521.549 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLAMFLGFLCAAGSTWGATSMALTV 29

Scoring table: BLOSUM62

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Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109.5	78.8	856	6	US-10-510-947-8
2	109.5	78.8	856	7	US-11-042-988-13
3	109.5	78.8	856	7	US-11-135-235-1
4	104.5	75.2	601	7	US-11-014-842A-37
5	104.5	75.2	613	7	US-11-014-842A-33
6	104.5	75.2	669	7	US-11-014-842A-29
7	104.5	75.2	681	7	US-11-014-842A-25
8	104.5	75.2	789	7	US-11-014-842A-39
9	104.5	75.2	801	7	US-11-014-842A-35
10	104.5	75.2	854	7	US-11-022-562-219
11	104.5	75.2	857	7	US-11-014-842A-31
12	104.5	75.2	869	7	US-11-014-842A-27
13	99.5	71.6	35	7	US-11-096-725-35
14	84	60.4	28	7	US-11-223-699A-96
15	84	60.4	28	7	US-11-121-566A-96
16	84	60.4	30	6	US-10-923-112A-30
17	79	56.8	21	7	US-11-078-256-288
18	79	56.8	27	6	US-10-985-426-3
19	79	56.8	27	7	US-11-067-092A-11
20	79	56.8	27	7	US-11-016-542-5
21	77	55.4	17	6	US-10-923-112A-29
22	77	55.4	17	7	US-11-223-699A-7
23	77	55.4	17	7	US-11-121-566A-7
24	74	53.2	15	7	US-11-045-024-12977
25	73.5	52.9	28	7	US-11-141-725-14

26	73	52.5	17	6	US-10-923-112A-28
27	71	51.1	15	7	US-11-045-024-12877
28	71	51.1	879	7	US-11-022-562-340
29	70	50.4	15	7	US-11-045-024-12943
30	69	49.6	15	7	US-11-045-024-12986
31	68	48.9	15	7	US-11-045-024-12869
32	66	47.5	860	7	US-11-022-562-217
33	65	46.8	20	7	US-11-022-562-176
34	56.5	40.6	15	7	US-11-045-024-12980
35	55	39.6	11	7	US-11-045-024-948
36	55	39.6	11	7	US-11-045-024-950
37	55	39.6	11	7	US-11-045-024-8467
38	54	38.8	11	7	US-11-045-024-951
39	54	38.8	11	7	US-11-045-024-8820
40	52	37.4	11	7	US-11-045-024-947
41	52	37.4	11	7	US-11-045-024-8424
42	51	36.7	10	7	US-11-045-024-817
43	51	36.7	10	7	US-11-045-024-8454
44	51	36.7	11	7	US-11-045-024-949
45	51	36.7	11	7	US-11-045-024-8604

ALIGNMENTS

RESULT 1

US-10-510-947-8
; Sequence 8, Application US/10510947
; Publication No. US20050255123A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Medina, Maria Fe C.
; APPLICANT: Kobinger, Gary
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor
; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; PRIOR FILING DATE: 2004-10-28
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/385,704
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 60/427,752
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-510-947-8

Query Match 78.8%; Score 109.5; DB 6; Length 856;
Best Local Similarity 82.8%; Pred. No. 5.2e-07;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Oy 1 AVGMGLAMFLGFLCAAGSTWGATSMALTV 29
Db 512 AVG-IGALFLGFLCAAGSTWGATSMALTV 539

RESULT 2

US-11-042-988-13
; Sequence 13, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; TITLE OF INVENTION: DRUG RESISTANCE
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988

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; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-042-988-13

Query Match      78.8%; Score 109.5; DB 7; Length 856;
Best Local Similarity 82.8%; Pred. No. 5.2e-07;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTWGAATSMALTIV 29
Db 512 AVG-IGALFLGFLGAAGSTWGAATSMALTIV 539

RESULT 3
US-11-135-235-1
; Sequence 1, Application US/11135235
; Publication No. US20060019395A1
; GENERAL INFORMATION:
; APPLICANT: Matasco, Wayne
; TITLE OF INVENTION: Lentiviral Vectors and Uses Thereof
; FILE REFERENCE: 20363-027
; CURRENT APPLICATION NUMBER: US/11/135,235
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 60/589,610
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-135-235-1

Query Match      78.8%; Score 109.5; DB 7; Length 856;
Best Local Similarity 82.8%; Pred. No. 5.2e-07;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTWGAATSMALTIV 29
Db 512 AVG-IGALFLGFLGAAGSTWGAATSMALTIV 539

RESULT 4
US-11-014-842A-37
; Sequence 37, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 37
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1

Query Match      75.2%; Score 104.5; DB 7; Length 601;
Best Local Similarity 79.3%; Pred. No. 1.6e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTWGAATSMALTIV 29
Db 442 AVG-IGAVFLGFLGAAGSTWGAATSMALTIV 469

RESULT 6
US-11-014-842A-29
; Sequence 29, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 29
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1

Query Match      75.2%; Score 104.5; DB 7; Length 613;
Best Local Similarity 79.3%; Pred. No. 1.6e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTWGAATSMALTIV 29
Db 442 AVG-IGAVFLGFLGAAGSTWGAATSMALTIV 469
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US-11-014-842A-29

Query Match 75.2%; Score 104.5; DB 7; Length 669;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 498 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 525

RESULT 7

US-11-014-842A-25

; Sequence 25, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 25

; LENGTH: 681

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-25

Query Match 75.2%; Score 104.5; DB 7; Length 681;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 510 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 537

RESULT 8

US-11-014-842A-39

; Sequence 39, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 39

; LENGTH: 789

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-39

Query Match 75.2%; Score 104.5; DB 7; Length 854;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Query Match 75.2%; Score 104.5; DB 7; Length 789;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 430 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 457

RESULT 9

US-11-014-842A-35

; Sequence 35, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 35

; LENGTH: 801

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-35

Query Match 75.2%; Score 104.5; DB 7; Length 801;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 442 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 469

RESULT 10

US-11-022-562-219

; Sequence 219, Application US/11022562

; Publication No. US20050249742A1

; GENERAL INFORMATION:

; APPLICANT: Ruprecht, Ruth M.

; APPLICANT: Shisong, Jiang

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE

; FILE REFERENCE: DFN-043CN

; CURRENT APPLICATION NUMBER: US/11/022,562

; CURRENT FILING DATE: 2004-12-22

; PRIOR APPLICATION NUMBER: PCT/US03/20322

; PRIOR FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: 60/392718

; PRIOR FILING DATE: 2002-06-27

; NUMBER OF SEQ ID NOS: 340

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 219

; LENGTH: 854

; TYPE: PRT

; ORGANISM: Human Immunodeficiency Virus

US-11-022-562-219

Query Match 75.2%; Score 104.5; DB 7; Length 854;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
||| :||:|||||:|||||:| :|||
Db 510 AVG-IGAVFLGFLGAAGSTMGAAASVILTV 537

RESULT 11
US-11-014-842A-31
; Sequence 27, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 31
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-31

Query Match 75.2%; Score 104.5; DB 7; Length 857;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
||| :||:|||||:|||||:| :|||
Db 498 AVG-IGAVFLGFLGAAGSTMGAAASVILTV 525

RESULT 12
US-11-014-842A-27
; Sequence 27, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 27
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-27

Query Match 75.2%; Score 104.5; DB 7; Length 869;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
||| :||:|||||:|||||:| :|||
Db 510 AVG-IGAVFLGFLGAAGSTMGAAASVILTV 537

RESULT 13
US-11-096-725-35
; Sequence 35, Application US/11096725
; Publication No. US20060013820A1
; GENERAL INFORMATION:
; APPLICANT: BONNET, Dominique
; APPLICANT: BROWN, Carlton B
; APPLICANT: GEORGES, Bertrand
; APPLICANT: SIZER, Philip J
; TITLE OF INVENTION: Antigen Delivery Vectors and Constructs
; FILE REFERENCE: KLB-001
; CURRENT APPLICATION NUMBER: US/11/096,725
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: GB0408164.2
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-096-725-35

Query Match 71.6%; Score 99.5; DB 7; Length 35;
Best Local Similarity 88.0%; Pred. No. 3.1e-07;
Matches 22; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 AVGMGLGAMFLGFLGAAGSTMGATSM 25
||| :||:|||||:|||||:| :|||
Db 11 AVG-IGAVFLGFLGAAGSTMGAAASM 34

RESULT 14
US-11-223-699A-96
; Sequence 96, Application US/11223699A
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; TITLE OF INVENTION: RIBONUCLEIC ACID TO A CELL
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: 11/121,566
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 96
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-223-699A-96

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Query Match 60.4%; Score 84; DB 7; Length 28;
Best Local Similarity 89.5%; Pred. NO. 2.6e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GAMFLGFLGAAGSTMGATS 24
|||:|||||||
Db 1 GAFGLGFLGAAGSTMGAWS 19

RESULT 15

US-11-121-566A-96
; Sequence 96, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; TITLE OF INVENTION: OF TARGET GENES IN CELLS

FILE REFERENCE: 04-0308
CURRENT APPLICATION NUMBER: US/11/121,566A
CURRENT FILING DATE: 2005-05-04

PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/656,572
PRIOR FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 60/667,633

; PRIOR APPLICATION NUMBER: 60/615, 912
 ; PRIOR FILING DATE: 2004-09-27
 ; PRIOR APPLICATION NUMBER: 60/570, 512
 ; PRIOR FILING DATE: 2004-05-12

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:32 ; Search time 262.28 Seconds
(without alignments)
1087.222 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474

Sequence: 1 ANLWTVYVYGVVWKEATTT.....ONQEKVQQLQLDKWASL 649

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3457	99.5	649	2 AAW44250	Aaw44250 HIV-1 gp1
2	3388	97.5	865	2 AAW43072	Aaw43072 HIV-1 gp1
3	2987	86.0	862	9 AEB10584	Aeb10584 Clade B e
4	2977.5	85.7	883	4 AAB82761	Aab82761 Ancestral
5	2977.5	85.7	883	9 ADW38347	Adw38347 Ancestral
6	2977.5	85.7	883	9 ADY27998	Ady27998 HIV-1 gro
7	2977.5	85.7	883	9 AEB10654	Aeb10654 ANI-EnvB
8	2977.5	85.7	883	9 AEB10552	Aeb10552 HIV-1, su
9	2970	85.5	850	9 ADZ07749	Adz07749 HIV subty
10	2949	84.9	862	9 AEB10583	Aeb10583 Clade B e
11	2947	84.8	842	9 ADY99903	Ady99903 Human cod
12	2947	84.8	1068	9 ADY99925	Ady99925 Human cod
13	2947	84.8	2602	9 ADY99929	Ady99929 Human cod
14	2939.5	84.6	841	9 ADZ07752	Adz07752 HIV CON-B
15	2937.5	84.3	841	9 ADZ07794	Adz07794 HIV CON-B
16	2922	84.1	840	9 ADZ07797	Adz07797 HIV B anc.
17	2891.5	83.2	856	6 ABR55495	Abr55495 Amino aci
18	2883.5	83.0	842	6 ABR55684	Abr55684 HIV isola
19	2883.5	83.0	842	7 ADC13218	Adc13218 Protein o
20	2883.5	83.0	842	9 ADW48030	Adw48030 HIV strai
21	2883.5	83.0	847	3 AAY97073	Aay97073 Variant H
22	2883.5	83.0	847	8 ADO05103	Ado05103 Human imm
23	2883.5	83.0	847	9 ADZ82338	Adz82338 HIV-1 pol
24	2878.5	82.9	842	6 ABU66565	Abu66565 Human imm

25	2876.5	82.8	842	8 ADM73868	Adm73868 HIV-1 pol
26	2870.5	82.6	842	5 ABB06211	Abb06211 HIV Env 1
27	2869.5	82.6	843	9 ADX39692	Adx39692 HIV Env p
28	2867.5	82.5	842	9 ADZ04164	Adz04164 Env prote
29	2852	82.1	850	2 AAR67724	Aar67724 Sp120 fro
30	2849.5	82.0	847	8 ADK14406	Adk14406 HIV wild-
31	2849.5	82.0	847	8 ADP20081	Adp20081 Human imm
32	2845.5	81.9	847	8 ADK14404	Adk14404 HIV mutan
33	2845	81.9	856	9 ADX39677	Adx39677 HIV Env p
34	2844	81.9	856	9 ADX39681	Adx39681 HIV Env p
35	2843.5	81.9	847	8 ADK14405	Adk14405 HIV mutan
36	2840.5	81.8	791	9 ADX39690	Adx39690 HIV Env p
37	2836.5	81.6	855	9 ADX39676	Adx39676 HIV Env p
38	2834	81.6	855	2 AAW11581	Aaw11581 Human imm
39	2834	81.6	855	2 AAW88113	Aaw88113 Env prote
40	2831.5	81.5	855	9 ADX39674	Adx39674 HIV Env p
41	2827.5	81.4	643	4 AAB61505	Aab61505 HIV-1 SOS
42	2827.5	81.4	643	6 ABR57052	Abr57052 HIV-1 JR-
43	2827.5	81.4	643	7 ADF18107	Adf18107 HIV-1 JR-
44	2827.5	81.4	643	8 ADK14399	Adk14399 HIV gp140
45	2827.5	81.4	643	8 ADU22853	Adu22853 HIV-1 JR-

ALIGNMENTS

RESULT 1
AAW44250
ID AAW44250 standard; protein; 649 AA.
XX
AC AAW44250;
XX
DT 17-OCT-2003 (revised)
DT 26-JUN-1998 (first entry)
XX
XX HIV-1 gp160 residues 33-681.
XX
XX Vaccine; antibody; antigen; hydrophobic; proteosome; pathogen;
XX immune response; sexually transmitted disease; HIV; infection.
XX Human immunodeficiency virus 1.
XX
XX Key Location/Qualifiers
XX Region 491..519
XX /note= "hydrophobic region"
XX
XX WO9801558-A2.
XX
PD 15-JAN-1998.
XX
XX 10-JUL-1997; 97MO-US012253.
XX
XX 10-JUL-1996; 96US-0021687P.
XX
XX (INTE-) INTELLIVAX INC.
XX (JACK-) JACKSON FOUND HENRY M.
XX (USSA) US SEC OF ARMY.
XX
XX Lowell GH, Vancott TC, Birx DL;
XX WPI; 1998-110231/10.
XX
XX Vaccine compositions for eliciting neutralising antibodies - comprising
XX antigen containing hydrophobic sequence or having added hydrophobic
XX material, complexed to proteosomes or bio-adhesive nano-emulsions.
XX
XX Claim 9; Page 22; 62pp; English.
XX
XX The present sequence represents HIV-1 gp160 residues 33-681 (the full
XX protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine
XX of the present invention. The vaccine composition is capable of eliciting
XX neutralising antibodies in a subject to a pathogenic organism which
XX antibodies are present in vaginal secretions, intestinal secretions, lung

CC secretions or faeces. The vaccine comprises: (a) an antigen comprising a
CC protein or peptide having: (i) an endogenous hydrophobic sequence of 3-50
CC non-polar or uncharged amino acids; (ii) added to the protein or peptide,
CC an exogenous hydrophobic material comprising a sequence of 3 to 50 non-
CC polar or uncharged amino acids or a 8-18C fatty acyl group, or (iii) both
CC (i) and (ii), and (b) complexed with the antigen, a composition
CC comprising proteosomes, bioadhesive nano-emulsions or both, where the
CC complexed or coupled protein or peptide maintains a native structure of
CC antigenic epitopes such that, upon administration to the subject, the
CC antigen induces neutralising antibodies in one or more of vaginal,
CC secretions, intestinal secretions, lung secretions and faeces, capable of
CC neutralising the pathogenic organism. The compositions can be used for
CC inducing an immune response against a pathogenic organism such as a
CC causative agent of a sexually-transmitted or mucosally-transmitted
CC disease, e.g. HIV infection. The compositions preserve the antigenic
CC integrity of the protein or peptide epitopes while at the same time
CC enhancing their immunogenicity. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 649 AA;

Query Match 99.5%; Score 3457; DB 2; Length 649;
Best Local Similarity 99.5%; Pred. No. 7.9e-187;
Matches 646; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANLWVTVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVTPNPNQEVVLENVTE 60
DB 1 ANLWVTVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVTPNPNQEVVLENVTE 60
QY 61 NFNMKNMVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVV 120
DB 61 NFNMKNMVAQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVV 120
QY 121 EQRKGEMRNCSENIITTSIRDKVQREYALFYKLDVEPIDNKNVTNTTKRLINCNTSVI 180
DB 121 EQRKGEMRNCSENIITTSIRDKVQREYALFYKLDVEPIDNKNVTNTTKRLINCNTSVI 180
QY 181 TQACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGRIPVVSQTLL 240
DB 181 TQACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGRIPVVSQTLL 240
QY 241 NGLSABEVVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 300
DB 241 NGLSABEVVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 300
QY 301 LGRNQAHCHISRAQWNNTLQIATTLREQFGNKTIAPNOSGDDPEIVMHSFNCGEFF 360
DB 301 LGRNQAHCHISRAQWNNTLQIATTLREQFGNKTIAPNOSGDDPEIVMHSFNCGEFF 360
QY 361 YCNSTQLFNSAWNTSNGTWSVTRKQDGTGDIITLPCRIKOIINRWQVGVKAMVALPIKG 420
DB 361 YCNSTQLFNSAWNTSNGTWSVTRKQDGTGDIITLPCRIKOIINRWQVGVKAMVALPIKG 420
QY 421 LIRCSSNITGLLTRDGGNGQTTEIPRPGGDMRDNWRSELYKYKVKIEPLGVAPTKA 480
DB 421 LIRCSSNITGLLTRDGGNGQTTEIPRPGGDMRDNWRSELYKYKVKIEPLGVAPTKA 480
QY 481 KRRVQREKAVGMLGNMFLGFLGAGSTWGTSMALTVOARQLLSGIVQQNNLLRAIK 540
DB 481 KRRVQREKAVGMLGNMFLGFLGAGSTWGTSMALTVOARQLLSGIVQQNNLLRAIK 540
QY 541 AQOHLQLTVWGIKQIQLARILAVERYLKQQLLGFVGCSCGLICTTAVPNWASWSNKTLD 600
DB 541 AQOHLQLTVWGIKQIQLARILAVERYLKQQLLGFVGCSCGLICTTAVPNWASWSNKTLD 600
QY 601 QIWNMTWMDREIDNYTHLIVTLIESQNKQEQQLQLDQWASL 649
DB 601 QIWNMTWMDREIDNYTHLIVTLIESQNKQEQQLQLDQWASI 649

RESULT 2
AAW43072
ID AAW43072 standard; peptide; 865 AA.

XX AAW43072;
AC
XX
DT 17-OCT-2003 (revised)
DT 11-SEP-1998 (first entry)
XX
DE HIV-1 gp120 protein fragment from isolate CDC4.
XX
KW gp120 protein; purification; fractionation; ion exchange; chromatography;
KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.
XX Human immunodeficiency virus 1.
OS
XX
XX US5696238-A.
XX
PD 09-DEC-1997.
XX
XX 11-MAY-1995; 95US-00439286.
XX
XX 20-AUG-1991; 91US-00684963.
XX 16-AUG-1993; 93US-00109002.
XX 09-MAY-1994; 94US-00240073.
XX
PA (CHIR) CHIRON CORP.
XX
XX Scandella C, Haigwood NL;
PI
XX
DR WPI; 1998-041353/04.
XX
PT Purification of HIV gp120 - using chromatographic methods.
XX
XX
PS Disclosure; Fig 2A-W; 53pp; English.
XX
CC AAW43066-W43080 are fragments of the gp120 protein from different human
CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used
CC in a novel method for purifying HIV gp120 so as to provide a purified
CC gp120 glycoprotein having protein/protein binding properties
CC substantially identical to natural viral HIV gp120. The method involves
CC fractionating a crude gp120 preparation containing full-length,
CC glycosylated gp120 using ion exchange chromatography so as to provide a
CC first collection of fractions. A fraction from the first collection is
CC selected that exhibits specific binding affinity for CD4 peptide, thereby
CC producing a first fractionated material. The first fractionated material
CC is fractionated by hydrophobic interaction chromatography so as to
CC provide a second collection of fractions from which a second collection
CC is selected that exhibits specific binding affinity for CD4 peptide. This
CC second fraction is fractionated by size exclusion chromatography so as to
CC provide a third collection of fractions exhibiting specific binding
CC affinity for CD4 peptide, thereby providing the purified gp120. The
CC purified gp120 can be used for antibody production and in vaccines.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 865 AA;

Query Match 97.5%; Score 3388; DB 2; Length 865;
Best Local Similarity 98.9%; Pred. No. 7.8e-183;
Matches 644; Conservative 1; Mismatches 0; Indels 6; Gaps 6;

QY 1 ANLWTVTVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVTPNPNQEVVLENVTE 60
DB 32 ANLWTVTVYGVVWKEA-TTLCASDAKAYDTEAHNVWATHACVTPNPNQEVVLENVTE 90
QY 61 NFNMKNMVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVV 119
DB 91 NFNMKNMVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVV 150
QY 120 WEORGKEMRNCSENIITTSIRDKVQREYALFYKLDVEPIDNKNV-TTNTTKRLINCNTS 178
DB 151 WEORGKEMRNCSENIITTSIRDKVQREYALFYKLDVEPIDNKNVDITNTTKRLINCNTS 210
QY 179 VITQACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGRIPVVSQT 238
DB 211 VITQACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGRIPVVSQT 270

QY 239 LLNGSLAEEVVRSENFNNNAKIIIVQLNVSVSEINCTRPNNHTRKRVTLPGRVWYTTG 298
 DB 271 LLNGSLAEEVVRSENFNNNAKIIIVQLNVSVSEINCTRPNNHTRKRVTLPGRVWYTTG 330
 QY 299 EILGNIRQAHCHNISRAQNNNTLQIATTLREQFGNKIIAFNQSNGGDPPIVHHSFNCGGE 358
 DB 331 QILGNIRQAHCHNISRAQNNNTLQIATTLREQFGNKIIAFNQSNGGDPPIVHHSFNCGGE 390
 QY 359 FFYCNSTOLFNSAWNVTSGTWSVTRKQKOTGDIITLPCRIKQIINRWQVVGKAMYALPI 418
 DB 391 -FYCNSTOLFNSAWNVTSGTWSVTRKQKOTGDIITLPCRIKQ- INRWQVVGKAMYALPI 448
 QY 419 KGLIRCSNITGLLTRDGGENQTTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 478
 DB 449 KGLIRCSNITGLLTRDGGENQTTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 508
 QY 479 KAKRVVQREKRAVGMGLGAMFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 538
 DB 509 KAKRVVQREKRAVGMGLGAMFLGAGSTMGATSMALTVOARQLLSGIV-QQNNLLRA 567
 QY 539 IKAQCHLLQLTWGIGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWENKT 598
 DB 568 IKAQCHLLQLTWGIGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWENKT 627
 QY 599 LDQIWNMTWMEWDREIDNTHLYTLIEESQNOQKQELLQDKWASL 649
 DB 628 LDQIWNMTWMEWDREIDNTHLYTLIEESQNOQKQELLQDKWASL 678

RESULT 3
 AEB10584
 ID AEB10584 standard; protein; 862 AA.
 AC AEB10584;
 XX
 XX 25-AUG-2005 (first entry)
 DT
 DE Clade B env (gp160) protein, Bgpl60.lscot, SEQ ID NO: 51.
 XX
 XX Immune stimulation; diagnosis; gene therapy; viral infection; virucide;
 KW infection; HIV infection; anti-hiv; env protein.
 KW
 XX Synthetic.
 OS
 XX US2005137387-A1.
 XX
 XX 23-JUN-2005.
 PD
 XX 17-FEB-2004; 2004US-00780507.
 PF
 XX 18-FEB-2000; 2000US-0183659P.
 PR 16-FEB-2001; 2001US-00204204.
 PR 16-FEB-2001; 2001WO-US005288.
 PR 14-FEB-2003; 2003US-0447586P.
 XX
 XX (UNIW) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF.
 PA
 XX Mullins JI, Rodrigo AG, Learn GH, Li F, Nickle DC, Jensen MA;
 XX WPI; 2005-444181/45.
 DR
 DR N-PSDB; AEB10561.
 XX
 XX New isolated ancestral or COT viral nucleic acid and amino acid sequences
 PT that are determined founder sequences of a highly diverse viral strain,
 PT useful for diagnosing, preventing or treating viral (e.g. HIV) infection.
 XX
 XX Claim 11; SEQ ID NO 51; 201pp; English.
 PS
 XX The invention relates to an ancestral or center of tree (COT) viral
 CC nucleic acid and amino acid sequences that are determined founder
 CC sequences of a highly diverse viral strain. The invention also relates to
 CC a composition comprising a highly diverse viral ancestor protein or an

CC immunogenic fragment of an ancestor or COT protein for inducing an immune
 CC response in a mammal and a method for preparing an ancestral or COT viral
 CC amino acid sequence. The composition and methods are useful for
 CC diagnosing, preventing or treating viral (e.g. HIV) infection. The
 CC invention is also useful in gene therapy. The present sequence is a clade
 CC B env (gp160) protein. This sequence is used in the comparison of the
 CC most recent common ancestor (MRCA), COT least squares (LScot) and COT
 CC minimum of means (MWCot) reconstructions for the clade B env gene.
 XX
 SQ Sequence 862 AA;

Query Match 86.0%; Score 2987; DB 9; Length 862;
 Best Local Similarity 86.6%; Pred. No. 3.1e-160;
 Matches 563; Conservative 31; Mismatches 46; Indels 10; Gaps 6;
 QY 3 LWTVYVGVVWKEATTTLCASDAKAYDTSAHVWATHACVPTNPQEVLENVTENF 62
 DB 33 LWTVYVGVVWKEATTTLCASDAKAYDTSAHVWATHACVPTNPQEVLENVTENF 92
 QY 63 NMKNNNVQVHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVWEQ 122
 DB 93 NMKNNNVQVHEDIISLWQSLKPCVKLTPLCVTLNCTDLN-KNATNTNSS---GEM 147
 QY 123 RGKGEWNCSEFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLNCNTSVITQ 182
 DB 148 MEKGEIKNCSEFNITTSIRDKVQREYALFYKLDVVPIDNNTNTNTTSYRLISCVITQ 207
 QY 183 ACPKVSPEPIPIHVCTPTGFALLKCNCKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG 242
 DB 208 ACPKVSPEPIPIHYCAPAGPAIILKCNCKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG 267
 QY 243 SLAEEVVRSENFNNNAKIIIVQLNVSVSEINCTRPNNHTRKRVTLPGRVWYTTGILG 302
 DB 268 SLAEEVVRSENFNNNAKIIIVQLNVSVSEINCTRPNNHTRKSIHIGGRAFYTTGILG 327
 QY 303 NIRQAHCHNISRAQNNNTLQIATTLREQFG-NKTIAFNQSNGGDPPIVHHSFNCGGEFFY 361
 DB 328 DIRQAHCHNISRAQNNNTLQIATTLREQFGNKIIAFNQSNGGDPPIVHHSFNCGGEFFY 387
 QY 362 CNSTOLFNSAWNVTSGTWSVTRKQKDT-GDITLPCRIKQIINRWQVVGKAMYALPIKG 420
 DB 388 CNSTOLFNSWNGT--WTWNTTGSNDTEGDTITLPCRIKQIINRWQVVGKAMYALPIRG 445
 QY 421 LIRCSSNITGLLTRDGGEN-QTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 479
 DB 446 QIRCSSNITGLLTRDGGNNNTNETEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 505
 QY 480 AKRVVQREKRAVGMGLGAMFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRAI 539
 DB 506 AKRVVQREKRAVGIIGAVFLGAGSTMGASMTLTVOARQLLSGIVQQNNLLRAI 565
 QY 540 KAOQHLLQLTWGIGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWENKT 599
 DB 566 KAOQHLLQLTWGIGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWENKT 625
 QY 600 DQIWNMTWMEWDREIDNTHLYTLIEESQNOQKQELLQDKWASL 649
 DB 626 DEIWNMTWMEWDREIDNTHLYTLIEESQNOQKQELLQDKWASL 675

RESULT 4
 AAB82761
 ID AAB82761 standard; protein; 883 AA.
 XX
 AC AAB82761;
 XX
 DT 11-SEP-2003 (revised)
 DT 29-OCT-2001 (first entry)
 XX
 XX Ancestral HIV-1 group M, subtype B gp160 protein.
 DE
 XX HIV-1; env gene; gp160 protein; ancestral gene; phylogeny; vaccine.
 KW

OS Human immunodeficiency virus 1.
 XX WO200160838-A2.
 XX
 XX
 XX
 XX PD 23-AUG-2001.
 XX
 XX PF 16-FEB-2001; 2001WO-US005288.
 XX
 XX PR 18-FEB-2000; 2000US-0183659P.
 XX
 XX PA (UNIW) UNIV WASHINGTON.
 XX
 XX PI Mullins JI, Rodrigo AG, Learn GH, Li F;
 XX
 XX DR WPI; 2001-536565/59.
 XX
 XX DR N-PSDB; AAH26468.
 XX
 XX PT Preparing an ancestral viral amino acid sequence useful as a vaccine
 PT comprises determining a recent ancestor of a circulating virus by maximum
 PT likelihood phylogeny analysis.
 XX
 XX PS Claim 8; Page 54; 89pp; English.
 XX
 CC The present sequence is that of an ancestral HIV-1 group M, subtype B
 CC gp160 (env gene product) sequence. The invention provides compositions
 CC and methods for determining ancestral viral gene sequences and ancestral
 CC viral protein sequences for highly diverse viruses, such as HIV-1. The
 CC methods use samples of circulating viruses to determine an ancestral
 CC viral sequence by maximum likelihood phylogeny analysis. In the present
 CC case, the ancestral HIV-1 subtype B env sequence (see AAH26468) was
 CC determined using 38 subtype B sequences (obtained from 9 different
 CC countries) and 3 subtype D (outgroup) sequences. The distances between
 CC this ancestral viral sequence and circulating strains used to determine
 CC it were on average 12.3% (range: 8.0-21.0%) while the available specimens
 CC were 17.3% different from each other (range: 13.3-23.2%). Thus, the
 CC ancestor sequence was, on average, more closely related to any given
 CC circulating virus than to any other variant. The ancestral gp160 sequence
 CC included a wide variety of immunogenically active peptides when processed
 CC for antigen presentation; nearly all known subtype B CTL epitope
 CC consensus amino acids were represented. Thus, an immunogenic composition
 CC to this subtype B ancestor protein will elicit broad neutralising
 CC antibody against HIV-1 isolates of the same subtype, and will also elicit
 CC a broad cellular response mediated by antigen-specific T-cells. A claimed
 CC vaccine composition comprises a viral ancestor protein or its immunogenic
 CC fragment, especially one derived from the HIV-1 group M subtype B gp160
 CC ancestral protein. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX SQ Sequence 883 AA;
 Query Match 85.7%; Score 2977.5; DB 4; Length 883;
 Best Local Similarity 84.7%; Pred. No. 1.1e-159;
 Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;
 3 LWTVVYGVVPWKEATTLFCASDAKAYDTAEHNVWATHACVPTNPNPQEVLENVTENF 62
 33 LWTVVYGVVPWKEATTLFCASDAKAYDTAEHNVWATHACVPTDNPQEVLENVTENF 92
 63 NMKNKNVVEQMHEDIISLWQSLKPCVKLPCLVTLNCTDLNNTNTNTTSLSIIVVWEQ 122
 93 NMKNKNVVEQMHEDIISLWQSLKPCVKLPCLVTLNCTDLNNTNTNTTSSATTNTS 152
 123 RG-----KGEMNCSEFNLTTSRDVKQREYALFYKLDVEPID-DNKNTNTNTKYRLIN 174
 153 SGGGTMEGEKGEIKNCSEFNLTTSRDVKQREYALFYKLDVVPIDNKNNTNTNTSRYLIN 212
 175 CNTSVITQACPKVSFEPIHYCTPTGTGTFALLKCNKDFNGTGPCTNVSTVQCTHGIRPVV 234
 213 CNTSVITQACPKVSFEPIHYCTPTGTFAGFALLKCNKDFNGTGPCTNVSTVQCTHGIRPVV 272
 235 STOLLNGLSLAEHVEVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRVW 294
 273 STOLLNGLSLAEHVEVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRAL 332

295 YTTGEILGNIROAHCMISRAQMNNTLQOIATTLREQFGNK--TIAFNQSSGGDPEIIVMHS 352
 333 YATGKIIGDIRQAHCLNSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIIVMHS 392
 353 FNCGGFFCYNSTQLFNSAMNVTSGTWSVTRKOK-----DTGDIITLPCRKIQIINRWQ 407
 393 FNCGGFFCYNSTQLFNSAMNVTSGTWSVTRKOK-----DTGDIITLPCRKIQIINRWQ 450
 408 VVGKAMVALPIKGLIRCSSNITGLLITRDGGENQOT-----TEIFRPGGDMRDNWRSELY 463
 451 EVGKAMYAPPISGOIRCSSNITGLLITRDGGENQOT-----TEIFRPGGDMRDNWRSELY 510
 464 KYKVKIEPLGVAPTAKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQ 523
 511 KYKVKIEPLGVAPTAKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQ 570
 524 LLSGIVQQNNLLRAIKAAQOHLQLTGWGIKQIQAARILAVERYLKQOQLLGWFGCSGKLI 583
 571 LLSGIVQQNNLLRAIKAAQOHLQLTGWGIKQIQAARILAVERYLKQOQLLGWFGCSGKLI 630
 584 CTTAVPNASWSNKTLDIWNNTMTWEDREIDNYTHLYTLIESQOQEKQOELLQL 643
 631 CTTAVPNASWSNKTLDIWNNTMTWEDREIDNYTHLYTLIESQOQEKQOELLQL 690
 644 DKWASL 649
 691 DKWASL 696

RESULT 5
 ADW38347
 ID ADW38347 standard; protein; 883 AA.
 XX ADW38347;
 AC ADW38347;
 XX
 XX 24-MAR-2005 (first entry)
 DT
 XX
 DE Ancestral HIV-1 group M subtype B envelope (env).
 XX
 XX virucide; vaccine; diagnosis; FIV infection; envelope; env.
 XX Human immunodeficiency virus 1.
 OS
 XX
 XX WO2005001029-A2.
 PN
 XX
 XX 06-JAN-2005.
 PD
 XX
 XX 19-MAY-2004; 2004WO-US015816.
 PF
 XX
 XX 19-MAY-2003; 2003US-00441926.
 PR
 XX
 XX (AUCK-) AUCKLAND UNISERVICES LTD.
 PA
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 XX Mullins JI, Rodrigo A, Ross HA;
 PI
 XX
 XX WPI; 2005-075527/08.
 DR
 XX N-PSDB; ADW38346.
 DR
 XX
 XX New ancestral feline immunodeficiency virus (FIV) nucleic acid sequence
 XX or its fragment that is a determined founder sequence of a highly diverse
 XX viral strain, subtype or group, useful in preparing a vaccine against
 XX FIV.
 XX
 XX Disclosure; SEQ ID NO 2; 225pp; English.
 PS
 XX
 XX The invention describes a new isolated ancestral feline immunodeficiency
 XX virus (FIV) nucleic acid sequence or its fragment is a determined founder
 XX sequence of a highly diverse viral strain, subtype or group. Also
 XX described are: an isolated ancestor protein or its fragment from FIV; an
 XX isolated expression construct comprising the operably linked elements
 XX consisting of a transcriptional promoter, a nucleic acid encoding an FIV
 XX ancestor protein and a transcriptional terminator; a cultured prokaryotic

or eukaryotic cell transformed with the expression construct; a composition for inducing an immune response in a mammal comprising a highly diverse FIV ancestor protein or its antigenic fragment; a method of preparing an FIV viral amino acid sequence; a method for inducing an immune response to FIV in a host; a method for making an FIV vaccine; a kit comprising a composition comprising an FIV ancestor protein or an antigenic fragment of an FIV ancestor protein and instructions for administering the composition to a subject; and a method for detecting infection with FIV. The ancestral feline immunodeficiency virus (FIV) nucleic acid sequence is useful in preparing a vaccine against FIV. This is the amino acid sequence of ancestral HIV-1 group M subtype B envelope (env) protein.

Sequence 883 AA;

Sequence 883 AA:

Query Match 85.7%; Score 2977.5; DB 9; Length 883;

Query Match	85.7%;	Score 2977.5;	DB 5
Best Local Similarity	84.7%;	Pred. No. 1.1e-159;	

Best Local Similarity	84.7%;	Pred. No. 1.1e-159;
Matches	564;	Conservative
Mismatches	27;	Mismatches
Indels	21;	Gaps

Qy	3	LWTVVYGVVWKEATITLFCASDAKAYDTEAHNVWATHACVPTNPNOEVLNVTFN	62
Db	33	LWTVVYGVVWKEATITLFCASDAKAYDTEAHNVWATHACVPTNPNOEVLNVTFN	92
Qy	63	NWKNMVEQHEHDIISLDOSLKPCKVLPCLVTNLCTDLNTNTNTTELSIIVWQ	122
Db	93	NWKNMVEQHEHDIISLDOSLKPCKVLPCLVTNLCTDLNTNTNTSSATNTTS	152
Qy	123	RG-----KGBMRCSFNITTSIRDKVOREYALFYKLDVEPID-DKNNTTNTKVR	174
Db	153	SGGTWGEKEIKNCSFNVTTSIRDKQKEYALFYKLDVVPIDNNTNTNTSVRLIN	212
Qy	175	CNTSVITQACPKVSEPIPIHYCTPTGFALLKCNCKXFNCTGCTNVSTVQCTHGIRPV	234
Db	213	CNTSVITQACPKVSEPIPIHYCTPAGFALLKCNCKXFNCTGCTNVSTVQCTHGIRPV	272
Qy	235	STOLLINGSLABEEVIRSEFTNAKTIIVOLNVSEINCTRPNNHTRKRVTLGPRVW	294
Db	273	STOLLINGSLABEEVIRSEFTNAKTIIVOLNVSEINCTRPNNHTRKRVTLGPRAL	332
Qy	295	YTTGILGNIROAHCHNISRAOWNTLOQIATLREOFGNK--TIAFNQSSGGDPEIVMHS	352
Db	333	YATGKIIGDIRQAHCHNRAKWNLTQIYTKUREQFGNNKTIIVFNQSSGGDPEIVMHS	392
Qy	353	FNCGGEFFYCNSTOLFNSAMNVTSNGTWSVTRKQK-----DTGDIITLPCR	407
Db	393	FNCGGEFFYCNSTOLFNSWTF--NGTWGNNTNTERSNAADDNDTITLPCR	450
Qy	408	VVGKAMYALPIKGLIRCSNITGLLLTRDGGENQT----TEIFRPGGDMRDNRS	463
Db	451	EVGKAMYAPPISGQIRCSNITGLLLTRDGGNNENTNTDTEIFRPGGDMRDNRS	510
Qy	464	KTKVKYIPELGVAPTKAKRRVQREKAVGMLGMFLGFLGAAGSTWGTATSVQARQ	523
Db	511	KTKVKYIPELGVAPTKAKRRVQREKAVGMLGMFLGFLGAAGSTWGAASMTLVQARQ	570
Qy	524	LLSGIVQOQNLLRAIKAOQHLLQITWYGIKQIARILAVERYLKQQLLGFPGWCSGKLI	583
Db	571	LLSGIVQOQNLLRAIEAQHLLQITWYGIKQIARVLAVERYLKQQLLGFPGWCSGKLI	630
Qy	584	CTTAVPNWASNKTLDOIWNNTMTWEDREINDYTHLIYTLLEESQOQEKQOELLQ	643
Db	631	CTTAVPNWASNKSLDKIWNNTMTWEWEREIDNYTGLIYTLLEESQOQEKQOELLQ	690
Qy	644	DKWASL 649	
Db	691	DKWASL 696	

RESULT 6

ADY27998

ID ADY27998 standard; protein; 883 AA.

XX
DEC 17 1964

AC ADY27998;

[illegible]

Query Match 85.7%; Score 2977.5; DB 9; Length 883;

Query Match 63.7%; Score 2577.5; DB
Best Local Similarity 84.7%; Pred. No. 1.1e-159;

	BEST LOCAL SIMILARITY	84.7%	PRED. NO.	I.IE-I59;
	MATCHES	564;	CONSERVATIVE	27;
	MISMATCHES	54;	INDELS	21;
	GAPS	6;		

Matches 364; Conservative 27; Mismatches 54; Index 21; Gaps 6;

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QY 3 LWTVTYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVLENVTENF 62
Db 33 LWTVTYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVLENVTENF 92
QY 63 NMWKNVVEQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVWEQ 122
Db 93 NMWKNVVEQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTSSATTNTTS 152
QY 123 RG-----KGMNRCSFNITTSIRDKVQREYALFYKLDVEPID-DNKNTTNNKTVRLIN 174
Db 153 SGGTMEGEKEIKNCSEFNVTTSIRDKKQKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
QY 175 CNTSVITQACPKVSFEPPIHYCTPTGFALLKNDKFKNGTGTCTNVSTVQCTHGIRPVV 234
Db 213 CNTSVITQACPKVSFEPPIHYCTPAGFAILKNDKFKNGTGTCTNVSTVQCTHGIRPVV 272
QY 235 STOLLINGSABEEVIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRW 294
Db 273 STOLLINGSABEEVIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKSIPIGGRAL 332
QY 295 YTTGEILGNIRQAHNCNISRAQWNTLQOIATTLREQFGNK--TIAFNQSSGGDPEIVMHS 352
Db 333 YATGKIIGDIRQAHNCNLSRAKWNNTLKQIVTKLREQFGNKTIVFNQSSGGDPEIVMHS 392
QY 353 FNCGGEFFYCNSTQLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKIINRWQ 407
Db 393 FNCGGEFFYCNSTQLFNSWHF--NGTWGNNTNTERSNNAADDNDTITLPCRKIINMWQ 450
QY 408 VVGKAMYPALPIKGLIRCSSNITGLLLTRDGGGENQF---TEIFRPGGDMRDNRSELY 463
Db 451 EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNENTNTTDEIFRPGGDMRDNRSELY 510
QY 464 KYKVKIEPLGVAPTAKERVVQREKAVGMLGAMFLGLAVERYLKQOQLLGFWGCSEGLI 583
Db 511 KYKVKIEPLGVAPTAKERVVQREKAVGMLGAMFLGLAVERYLKQOQLLGFWGCSEGLI 570
QY 524 LLSGIVQOQNLLRAIKAOQHLLQLTWGIKQIARILAVERYLKQOQLLGFWGCSEGLI 630
Db 571 LLSGIVQOQNLLRAIEAQHLLQLTWGIKQIARILAVERYLKQOQLLGFWGCSEGLI 643
QY 584 CTTAVPNASWNSKTLDOIWNNTWMEWDREIDNYTHLYTLIEESQOQEKNOQELLQL 643
Db 631 CTTAVPNASWNSKSLDKIWNNTWMEWEREIDNYTHLYTLIEESQOQEKNOQELLQL 690
QY 644 DKWASL 649
Db 691 DKWASL 696

RESULT 7
AEB10654
ID AEB10654 standard; protein; 883 AA.
XX AC
XX AEB10654;
DT 25-AUG-2005 (first entry)
XX DE
XX AN1-EnvB ancestor protein, SEQ ID NO: 121.
XX Immune stimulation; diagnosis; gene therapy; viral infection; virucide;
KW infection; HIV infection; anti-hiv; ancestor protein.
XX Synthetic.
XX US2005137387-A1.
XX PN
XX 23-JUN-2005.
XX PD
XX 17-FEB-2004; 2004US-00780507.
XX PF
XX 18-FEB-2000; 2000US-0183659P.
XX PR
XX 16-FEB-2001; 2001US-00204204.
XX PR
XX 16-FEB-2001; 2001WO-US0005288.
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PR 14-FEB-2003; 2003US-0447586P.
XX (UNIW ) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF.
PA Mullins JI, Rodrigo AG, Learn GH, Li P, Nickle DC, Jensen MA;
XX WPI; 2005-444181/45.
XX New isolated ancestral or COT viral nucleic acid and amino acid sequences
XX that are determined founder sequences of a highly diverse viral strain,
XX useful for diagnosing, preventing or treating viral (e.g. HIV) infection.
XX Example 8; SEQ ID NO 121; 201pp; English.
XX The invention relates to an ancestral or center of tree (COT) viral
XX nucleic acid and amino acid sequences that are determined founder
XX sequences of a highly diverse viral strain. The invention also relates to
XX a composition comprising a highly diverse viral ancestor protein or an
XX immunogenic fragment of an ancestor or COT protein for inducing an immune
XX response in a mammal and a method for preparing an ancestral or COT viral
XX amino acid sequence. The composition and methods are useful for
XX diagnosing, preventing or treating viral (e.g. HIV) infection. The
XX invention is also useful in gene therapy. The present sequence is an AN1-
XX EnvB ancestor protein.
SQ Sequence 883 AA;

Query Match 85.7%; Score 2977.5; DB 9; Length 883;
Best Local Similarity 84.7%; Pred. No. 1.1e-159;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

QY 3 LWTVTYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVLENVTENF 62
Db 33 LWTVTYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVLENVTENF 92
QY 63 NMWKNVVEQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVWEQ 122
Db 93 NMWKNVVEQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTSSATTNTTS 152
QY 123 RG-----KGMNRCSFNITTSIRDKVQREYALFYKLDVEPID-DNKNTTNNKTVRLIN 174
Db 153 SGGTMEGEKEIKNCSEFNVTTSIRDKMKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
QY 175 CNTSVITQACPKVSFEPPIHYCTPTGFALLKNDKFKNGTGTCTNVSTVQCTHGIRPVV 234
Db 213 CNTSVITQACPKVSFEPPIHYCTPAGFAILKNDKFKNGTGTCTNVSTVQCTHGIRPVV 272
QY 235 STOLLINGSABEEVIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRW 294
Db 273 STOLLINGSABEEVIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKSIPIGGRAL 332
QY 295 YTTGEILGNIRQAHNCNISRAQWNTLQOIATTLREQFGNK--TIAFNQSSGGDPEIVMHS 352
Db 333 YATGKIIGDIRQAHNCNLSRAKWNNTLKQIVTKLREQFGNKTIVFNQSSGGDPEIVMHS 392
QY 353 FNCGGEFFYCNSTQLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKIINRWQ 407
Db 393 FNCGGEFFYCNSTQLFNSWHF--NGTWGNNTNTERSNNAADDNDTITLPCRKIINMWQ 450
QY 408 VVGKAMYPALPIKGLIRCSSNITGLLLTRDGGGENQF---TEIFRPGGDMRDNRSELY 463
Db 451 EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNENTNTTDEIFRPGGDMRDNRSELY 510
QY 464 KYKVKIEPLGVAPTAKERVVQREKAVGMLGAMFLGLAVERYLKQOQLLGFWGCSEGLI 583
Db 511 KYKVKIEPLGVAPTAKERVVQREKAVGMLGAMFLGLAVERYLKQOQLLGFWGCSEGLI 570
QY 524 LLSGIVQOQNLLRAIKAOQHLLQLTWGIKQIARILAVERYLKQOQLLGFWGCSEGLI 630
Db 571 LLSGIVQOQNLLRAIEAQHLLQLTWGIKQIARILAVERYLKQOQLLGFWGCSEGLI 643
QY 584 CTTAVPNASWNSKTLDOIWNNTWMEWDREIDNYTHLYTLIEESQOQEKNOQELLQL 643
Db 631 CTTAVPNASWNSKSLDKIWNNTWMEWEREIDNYTHLYTLIEESQOQEKNOQELLQL 690
```

Db	631	CITAVPWNASWNSKSLDKIWNMTWMEWERIDNYTGLTYLTIEESQOQEKNEQELLE	690
Qy	644	DKWASL 649	
Db	691	DKWASL 696	
RESULT 8			
AEB10552			
ID	AEB10552 standard; protein; 883 AA.		
AC	AC		
AC	AEB10552;		
XX			
DT	25-AUG-2005 (first entry)		
XX			
DE	HIV-1, subtype B, env ancestor protein, SEQ ID NO: 2.		
XX			
KW	Immune stimulation; diagnosis; gene therapy; viral infection; virucide;		
KW	infection; HIV infection; anti-hiv; env ancestor protein.		
XX			
OS	Human immunodeficiency virus 1.		
XX			
PN	US2005137387-A1.		
XX			
PD	23-JUN-2005.		
XX			
PF	17-FEB-2004; 2004US-00780507.		
XX			
PR	18-FEB-2000; 2000US-0183659P.		
PR	16-FEB-2001; 2001US-00204204.		
PR	16-FEB-2001; 2001WO-US005288.		
PR	14-FEB-2003; 2003US-0447586P.		
XX			
PA	(UNIW) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSP.		
XX			
PI	Mullins JI, Rodrigo AG, Learn GH, Li P, Nickle DC, Jensen MA;		
XX			
DR	WPI; 2005-444181/45.		
DR	N-PSDB; AEB10551.		
PT			
PT	New isolated ancestral or COT viral nucleic acid and amino acid sequences		
PT	that are determined founder sequences of a highly diverse viral strain,		
PT	useful for diagnosing, preventing or treating viral (e.g. HIV) infection.		
XX			
PS	Claim 11; SEQ ID NO 2; 201pp; English.		
XX			
CC	The invention relates to an ancestral or center of tree (COT) viral		
CC	nucleic acid and amino acid sequences that are determined founder		
CC	sequences of a highly diverse viral strain. The invention also relates to		
CC	a composition comprising a highly diverse viral ancestor protein or an		
CC	immunogenic fragment of an ancestor or COT protein for inducing an immune		
CC	response in a mammal and a method for preparing an ancestral or COT viral		
CC	amino acid sequence. The composition and methods are useful for		
CC	diagnosing, preventing or treating viral (e.g. HIV) infection. The		
CC	invention is also useful in gene therapy. The present sequence is the		
CC	Human immunodeficiency virus 1 (HIV-1), subtype B, env ancestral protein.		
XX			
XX	Sequence 883 AA;		
Query Match 85.7%; Score 2977.5; DB 9; Length 883;			
Best Local Similarity 84.7%; Pred. No. 1.1e-159;			
Matches 564; Conservative . 27; Mismatches 54; Indels 21; Gaps 6			
Qy	3	LWTVVYGYGVVWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPNPQSVLENTENP	62
Db	33	LWTVVYGYGVVWKEATTTILFCASDAKAYDTEAHNVWATHACVPTDPPNPQSVLENTENP	92
Qy	63	NWKNKNVWQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLNTNTNTNTSILIVVWQ	122
Db	93	NWKNKNVWQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLDLRNATNTNTSSATNTTS	152
Qy	123	RG-----KGEWRNCSFNITTSIRDKVQREYALFYKLDVEPID-DKNKNTNNTKRLIN	174

Db	153	SGGTGMEGKEGIIKNCSEFNVTTSIRDKMCKEYALFYKLDVPIDNDNNNTNNTSYRLIN	211
Qy	175	CNTSVITQACPKVSEFPIPIHYCTPTGFALLKCDKFKFNGTGPCTNVSTVQCTHGIRPVV	234
Db	213	CNTSVITQACPKVSEFPIPIHYCTPAGFAILKCDKFKFNGTGPCTNVSTVQCTHGIRPVV	272
Qy	235	STOLLNGSLABEEVWIRSENFNTNAKTIIVQLNVSVSEINCTRPNNHTRKRVTLGPRVW	294
Db	273	STOLLNGSLABEEVWIRSENFNTNAKTIIVQLNESVEINCTRPNNNTRKSIPIGPRAL	332
Qy	295	YTTGEILGNIRQAHCHNSRACOWNNTLQOIATTLREQFGNK--TIAFNOSSGGDPPIVMHS	352
Db	333	YATGKIIGDIRQAHCHNSRAKWNNTLKQIVTKLREQFGNKTIVFNOSSGGDPPIVMHS	392
Qy	353	FNCGGFFPFCNSTQFNSANVTSNGTWSVTRKQK-----DTGDIITILPCRKQIINRWQ	407
Db	393	FNCGGFFPFCNSTQLFNSTWHF--NGTWGNNTNTERSNNAAADDNDTITILPCRKQIINMWQ	450
Qy	408	VVGKAMVALPKGLIRCSSNITGLLLTRDGGEGNQV-----TEIFRPGGDMRDNRSELY	463
Db	451	EVGKAMVAPPISGGIRCSSNITGLLLTRDGGNNENTNTTDEIFRPGGDMRDNRSELY	510
Qy	464	KYKVKLEPLGVAPTKAKRRVVQREKRAVGMGLGAMFLGLGAAGSTMGATSMALTIVQARQ	523
Db	511	KYKVKLEPLGVAPTKAKRRVVQREKRAVGMGLGAMFLGLGAAGSTMGAASMTLTVQARQ	570
Qy	524	LLSGIVQQNNLLRAIKAAQCHLLQITVWGIKQLQARILAVERYLKDQQLLGFPGWCGKLI	583
Db	571	LLSGIVQQNNLLRAIEAQCHLLQITVWGIKQLQARVLAVERYLKDQQLLGFPGWCGKLI	630
Qy	584	CTTAVPNWASNTLDOIWNNTWMEWDREIDNYTHLIYTLIEBSQOQEKQOQELLOL	643
Db	631	CTTAVPNWASNSKSLDKIWNNTWMEWERIDNYTGLIYTLIEBSQOQEKQOQELLEL	690
Qy	644	DKWASL 649	
Db	691	DKWASL 696	
RESULT 9			
ADZ07749			
ID	ADZ07749	standard; protein; 850 AA.	
XX	AC		
XX	AC		
XX	AC		
DT	16-JUN-2005	(first entry)	
XX			
DE	HIV subtype B consensus env protein.		
XX			
XX	anti-HIV; Immunoestimulant; immune stimulation; HIV infection; infection;		
KW	env.		
XX			
OS	Human immunodeficiency virus.		
XX			
FN	WO2005028625-A2.		
XX			
PD	31-MAR-2005.		
XX			
FF	17-SEP-2004; 2004WO-US030397.		
XX			
PR	17-SEP-2003; 2003US-0503460P.		
PR	27-AUG-2004; 2004US-0604722P.		
XX			
XX	(UYDU-) UNIV DUKE.		
PA	(KORB/) KORBER B T.		
PA	(HAHN/) HAHN B H.		
PA	(SHAW/) SHAW G M.		
PA	(KOTH/) KOTHE D.		
PA	(LIYV/) LI Y Y.		
PA	(DECK/) DECKER J.		
XX			
XX	Korber BT, Hahn BH, Shaw GM, Kothe D, Li YV, Decker J;		
PI	Haynes BF, Gao F, Liao H;		

Korber BT, Hahn BH, Shaw GM, Kothe D, Li YY, Decker J;
Haynes BF, Gao F, Liao H;

Db 490 RVVOREKRAVG-IGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 548
 QY 543 QHLLQLTWGKIKQOLARILAVERYLKDQQLGFWGCGSKLICTTAVPWNASWSNKTLDQI 602
 Db 549 QHLLQLTWGKIKQOLARILAVERYLKDQQLGFWGCGSKLICTTAVPWNASWSNKTLDQI 608
 QY 603 WNNMTWMEWDREIDNTHLYLTIIEESQNOQKQOELLQLDKWASL 649
 Db 609 WNNMTWMEWEREIDNTHLYLTIIEESQNOQKQOELLQLDKWASL 655

RESULT 12

ADY99925
 ID ADY99925 standard; protein; 1068 AA.

XX AC ADY99925;

XX DT 16-JUN-2005 (first entry)

XX DE Human codon-optimized HIV B Env-Nef fusion protein.

XX KW env; nef; fusion protein; viral replication; recombinant DNA; vector;
 KW vaccine; cancer; infectious disease; HIV; hepatitis;
 KW variola virus infection; immune stimulation; antimicrobial; virucide;
 KW anti-HIV; cytostatic; antiinflammatory; hepatotropic; immunogenicity.

XX OS Homo sapiens.

XX OS Human immunodeficiency virus 1.

XX PN WO2005028634-A2.

XX PD 31-MAR-2005.

XX PF 20-SEP-2004; 2004WO-US030849.

XX PR 18-SEP-2003; 2003US-0504030P.

XX PA (UYEM-) UNIV EMORY.

XX PI Feinberg MMD, Garber D;

XX DR WPI; 2005-254126/26.

XX DR N-PSDB; ADY99924.

XX PT New recombinant modified vaccinia Ankara virus comprising first null
 PT mutation in vaccinia gene, useful for treating or preventing viral
 PT infection (e.g. HIV, hepatitis and smallpox), and cancer.

XX PS Claim 69; SEQ ID NO 53; 324pp; English.

XX CC This invention relates to a novel recombinant modified vaccinia Ankara
 CC virus (rMVA). Specifically, it refers to the use of rMVA vectors in the
 CC development of vaccines to protect against cancer or infectious viral
 CC diseases such as HIV, hepatitis and smallpox. The present invention
 CC describes introducing a null mutation (preferably a deletion) into a
 CC vaccinia gene that is necessary for replication of the rMVA, in
 CC particular an exemplary gene is the vaccinia uracil DNA glycosylase gene.
 CC Additional vaccinia genes that can contain null mutations include, but
 CC are not limited to, ILI beta receptor, A46R, IL-18BP, A41L and E3L.
 CC Accordingly, it provides a system for producing an appropriate vaccine
 CC that involves an immortalized, non-transformed avian fibroblast cell
 CC infected with the rMVA, where the cell is from a complementing cell line
 CC that is engineered to express the gene necessary for viral replication,
 CC such that the virus is able to propagate. Furthermore, the rMVA may
 CC include a heterologous nucleic acid sequence encoding an antigen or a
 CC fragment thereof derived from viral, animal or plant polynucleotides, for
 CC example this may include an antigen from the HIV virus, measles virus,
 CC SARS virus, influenza virus, malaria plasmodium, tuberculosis Bacillus,
 CC yellow fever virus, dengue flavivirus or the river blindness nematode.
 CC The rMVA also comprises a second heterologous nucleic acid sequence
 CC encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably
 CC linked to an early stage viral promoter. As such, the developed vaccine

CC can be administered in a sufficient amount to effect an immune response
 CC in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic,
 CC antiinflammatory and hepatotropic activities. This polypeptide sequence
 CC is a human codon-optimized HIV-1 consensus fusion protein sequence,
 CC encoded by an antigenic sequence of an MVA-based vector given in an
 CC exemplification of the invention.

XX SQ Sequence 1068 AA;

Query Match 84.8%; Score 2947; DB 9; Length 1068;
 Best Local Similarity 86.2%; Pred. No. 6.6e-158;
 Matches 558; Conservative 25; Mismatches 40; Indels 24; Gaps 5;

QY 3 LMTVTYGVVPWKKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQSVLENVTENF 62

Db 33 LMTVTYGVVPWKKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQSVLENVTENF 92

QY 63 NMWKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTNTTTELSIIVVEQ 122

Db 93 NMWKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTNTTSSS---WET 146

QY 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 182

Db 147 MEKGEIKNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 199

QY 183 ACPKVSEPIPIHYCTPTGALIKCNDKKGNGTGPCTNVSTVQCTHGIRVWSTOLLNG 242

Db 200 ACPKVSEPIPIHYCAPAGFAILKNDKFGNGTGPCTNVSTVQCTHGIRVWSTOLLNG 259

QY 243 SLAEVEVIRSENFNTNAKTIIVQLNVSVIRNCTRNPNHTRKVTLPQPGVWVTTGILG 302

Db 260 SLAEVEVIRSENFNTNAKTIIVQLNVSVIRNCTRNPNHTRKVTLPQPGVWVTTGILG 319

QY 303 NIQAHCNISRAQNNNTLQOIATTLREQFNKNTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362

Db 320 DIRQAHCNISRAQNNNTLQOIVIKLREQFNKNTIAFNQSSGGDPEIVMHSFNCGGEFFYC 379

QY 363 NSTOLENSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKOIINRWVGVKAMYPKGLI 422

Db 380 NSTOLF-----TWNDTRKLNNTGRNITLPCRIKOIINRWVGVKAMYPKGLI 429

QY 423 RCSSNITGLLLTRDGGGNETEIFRPGGDMNDRSELYKYVKVKEPLGVAPTAKR 482

Db 430 RCSSNITGLLLTRDGGGNETEIFRPGGDMNDRSELYKYVKVKEPLGVAPTAKR 489

QY 483 RVVOREKRAVGMIGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 542

Db 490 RVVOREKRAVGMIGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 548

QY 543 QHLLQLTWGKIKQOLARILAVERYLKDQQLGFWGCGSKLICTTAVPWNASWSNKTLDQI 602

Db 549 QHLLQLTWGKIKQOLARILAVERYLKDQQLGFWGCGSKLICTTAVPWNASWSNKTLDQI 608

QY 603 WNNMTWMEWDREIDNTHLYLTIIEESQNOQKQOELLQLDKWASL 649

Db 609 WNNMTWMEWEREIDNTHLYLTIIEESQNOQKQOELLQLDKWASL 655

RESULT 13

ADY99929

ID ADY99929 standard; protein; 2602 AA.

XX AC ADY99929;

XX DT 16-JUN-2005 (first entry)

XX DE Human codon-optimized HIV B Gag-Pol-Env-Nef fusion protein.

XX KW gag; pol; env; nef; fusion protein; viral replication; recombinant DNA;
 KW vector; vaccine; cancer; infectious disease; HIV; hepatitis;
 KW variola virus infection; immune stimulation; antimicrobial; virucide;
 KW anti-HIV; cytostatic; antiinflammatory; hepatotropic; immunogenicity.

PS Disclosure; Fig 28A; 284pp; English.

XX The invention describes an isolated protein (I) selected from 106 fully
CC defined 500-866 amino acid sequences given in the specification. Also
CC described are: a nucleic acid comprising: a nucleotide sequence encoding
CC C06 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype
CC C consensus HIV envelope protein, subtype C consensus HIV gag protein,
CC subtype C consensus HIV nef protein, Group M consensus HIV envelope
CC protein, subtype A consensus HIV envelope protein, Group M consensus HIV
CC gag protein, Group M consensus HIV pol protein, Group M consensus HIV nef
CC protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag
CC protein, or subtype B consensus HIV envelope protein, where the
CC nucleotide sequence comprises codons optimized for expression in human
CC cells; a nucleotide sequence encoding (I); or a nucleotide sequence
CC selected from 89 fully defined 633-2607 bp sequences given in the
CC specification; a vector comprising the nucleic acid of (1); a composition
CC comprising at least one protein or nucleic acid above and a carrier; and
CC inducing an immune response in a mammal. The protein is a consensus or
CC ancestral immunogen useful for inducing antibodies that neutralize a wide
CC spectrum of HIV primary isolates and/or that induces a T cell response.
CC This is the amino acid sequence of a HIV (CON-B) consensus gp140 env
CC fusion protein.

XX SQ Sequence 841 AA;

Query Match 84.6%; Score 2939.5; DB 9; Length 841;
Best Local Similarity 86.1%; Pred. No. 1.4e-157;
Matches 557; Conservative 31; Mismatches 34; Indels 25; Gaps 7;

Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQHEHDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTSLIIVWVEQ 122
Db 93 NMWKNVVEQHEHDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTT---IIRW-- 147
Qy 123 RGKEMRNCSENIITSDKVOREYALFYKLDVPEIDDKNTNTKYLINCNTSVITQ 182
Db 148 --RGEIKNCSENIITSDKVOREYALFYKLDVPEIDN-----DNTSYRLISCNTSVITQ 200
Qy 183 ACPKVSFEPIHYCTPTGFALLKCNKFKNGTGCTNVSTVQCTHGIRPVSTQLLNG 242
Db 201 ACPKVSFEPIHYCAPAGPAILKCNKFKNGTGCTNVSTVQCTHGIRPVSTQLLNG 260
Qy 243 SLAEVWIRSENTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
Db 261 SLAEVWIRSENTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 320
Qy 303 NIRAHCNISRAQNNWTLQIATTLRQFGNKTAFNQSOGDPEIIVWHSFNCGGEFFYC 362
Db 321 DIRAHCNISRAQNNWTLQIATTLRQFGNKTAFNQSOGDPEIIVWHSFNCGGEFFYC 380
Qy 363 NSTQFNLSAMVNTSGTVTRKQKTDGDIITLPCRIKLIINRWQVVGKAMYPKIGLI 422
Db 381 NTTQLFNSTW---NGTWN-----NTEGNTLPCRIKLIINRWQVVGKAMYPKIGLI 430
Qy 423 RCSSNITGLLTRGGGSENTTEIFRPGGDMRNWSELYKYKVKIEPLGVAPTAKR 482
Db 431 RCSSNITGLLTRDGG--NNETEIFRPGGDMRNWSELYKYKVKIEPLGVAPTAKR 488
Qy 483 RVVQREKRAVGMGLGAMFLGFLGAGSTWGATSMALTVOARQLLSGIYQQNNLLRAKQ 542
Db 489 RVVQREKRAVG-IGAMFLGFLGAGSTWGATSMALTVOARQLLSGIYQQNNLLRAKQ 547
Qy 543 QHLLQLTWGIGKIQARILAVERYLKDQQLLGFQCSGKLICTTAVPWNASWSNKLDOI 602
Db 548 QHLLQLTWGIGKIQARILAVERYLKDQQLLGFQCSGKLICTTAVPWNASWSNKLDOI 607
Qy 603 WNNWTWEDWEIDNTHYLIIVTLIESQNOEKQVQELLQDKWASL 649
Db 608 WDNMTWWEWEIDNTHYLIIVTLIESQNOEKQVQELLQDKWASL 654

RESULT 15

ADZ07794
ID ADZ07794 standard; protein; 841 AA.
XX AC ADZ07794;
XX DT 16-JUN-2005 (first entry)
XX DE HIV CON-B env protein.
XX KW anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection;
XX KW CON-B; env; envelope.
XX OS Human immunodeficiency virus.
XX PN W02005028625-A2.
XX PD 31-MAR-2005.
XX PF 17-SEP-2004; 2004WO-US030397.
XX PR 17-SEP-2003; 2003US-0503460P.
XX PR 27-AUG-2004; 2004US-0604722P.
XX (UVDU-) UNIV DUKE.
PA (KORB/) KORBER B T.
PA (HAHV/) HAHN B H.
PA (SHAW/) SHAW G M.
PA (KOTH/) KOTHE D.
PA (LIYV/) LI Y Y.
PA (DECK/) DECKER J.
XX Korber BT, Hahn BH, Shaw GM, Kothe D, Li YY, Decker J;
PI Haynes BF, Gao F, Liao H;
XX WPI; 2005-242571/25.
DR N-PSDB; ADZ07796.
XX New isolated consensus or ancestral immunogenic proteins, useful for
PT inducing antibodies that neutralize a wide spectrum of human
PT immunodeficiency virus (HIV) primary isolates and/or that induces a T
PT cell response.
XX Claim 66; Fig 44A; 284pp; English.
XX The invention describes an isolated protein (I) selected from 106 fully
CC defined 500-866 amino acid sequences given in the specification. Also
CC described are: a nucleic acid comprising: a nucleotide sequence encoding
CC C06 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype
CC C consensus HIV envelope protein, subtype C consensus HIV gag protein,
CC subtype C consensus HIV nef protein, Group M consensus HIV envelope
CC protein, subtype A consensus HIV envelope protein, Group M consensus HIV
CC gag protein, Group M consensus HIV pol protein, Group M consensus HIV nef
CC protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag
CC protein, or subtype B consensus HIV envelope protein, where the
CC nucleotide sequence comprises codons optimized for expression in human
CC cells; a nucleotide sequence encoding (I); or a nucleotide sequence
CC selected from 89 fully defined 633-2607 bp sequences given in the
CC specification; a vector comprising the nucleic acid of (1); a composition
CC comprising at least one protein or nucleic acid above and a carrier; and
CC inducing an immune response in a mammal. The protein is a consensus or
CC ancestral immunogen useful for inducing antibodies that neutralize a wide
CC spectrum of HIV primary isolates and/or that induces a T cell response.
CC This is the amino acid sequence of HIV (CON-B) env protein.

SQ Sequence 841 AA;

Query Match 84.3%; Score 2927.5; DB 9; Length 841;
Best Local Similarity 85.9%; Pred. No. 6.8e-157;
Matches 556; Conservative 31; Mismatches 35; Indels 25; Gaps 7;
Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVPTNPQEVLENVTENF 62

[illegible]

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Job time : 268.28 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 7, 2006, 17:45:48 ; Search time 49.7758 Seconds
(without alignments)
1254.519 Million cell updates/sec
Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474
Sequence: 1 ANLWVTYYGVVWKEATTT.....ONQEKVQQLQLDKWASL 649
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3474	100.0	868	1 VCLJH4	env polyprotein -
2	2869.5	82.6	843	1 H44001	env polyprotein pr
3	2858	82.3	856	1 VCLJ3W	env polyprotein pr
4	2849.5	82.0	847	2 T09448	envelope glycoprot
5	2837	81.7	852	2 T12016	envelope glycoprot
6	2836.5	81.6	847	2 S13289	env protein - huma
7	2816.5	81.1	852	1 VCLJBR	env polyprotein -
8	2815.5	81.0	855	1 VCLJA2	env polyprotein pr
9	2809.5	80.9	854	2 S13288	env protein - huma
10	2808	80.8	729	1 VCLJFX	env polyprotein pr
11	2808	80.8	861	1 VCLJXB	env polyprotein pr
12	2806.5	80.8	856	1 VCLJH3	env polyprotein pr
13	2799.5	80.6	856	1 VCLJVL	env polyprotein pr
14	2795	80.5	861	1 VCLJLV	env polyprotein pr
15	2782	80.1	851	2 S33985	env polyprotein -
16	2765.5	79.6	861	1 VCLJSC	env polyprotein pr
17	2746	79.0	859	1 VCLJMN	env polyprotein pr
18	2623.5	75.5	853	2 S54384	env polyprotein pr
19	2616.5	75.3	855	1 VCLJZR	envelope polyprote
20	2566	73.9	846	1 VCLJND	env polyprotein pr
21	2550	73.4	856	1 A44963	env polyprotein pr
22	2516	72.4	859	2 T01672	envelope polyprote
23	2130.5	61.3	854	1 VCLJSI	env polyprotein pr
24	2074	59.7	506	2 A40218	envelop glycoprote
25	1909	55.0	495	2 S31493	env polyprotein -
26	1825	52.5	443	2 C41621	env polyprotein p
27	1802	51.9	445	2 A41621	env polyprotein M
28	1751.5	50.4	877	2 S49197	envelope protein p
29	1746.5	50.3	454	2 B41621	env polyprotein D

ALIGNMENTS

RESULT 1

VCLJH4
env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: C25523
R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human A:Reference number: A94136; MUID:87041461; PMID:3490666
A:Accession: C25523
A:Molecule type: DNA
A:Residues: 1-868 <DBS>
A:Cross-references: UNIPROT:P05879; UNIPARC:UPI0000012A014; GB:M13137; NID:g326460; PIDN:
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote F:1-521/Product: coat protein gp120 #status predicted <GPI>
F:522-868/Product: coat protein gp41 #status predicted <GPI>
F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459
Query Match 100.0%; Score 3474; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 6.4e-247; Indels 0; Gaps 0;
Matches 649; Conservative 0; Mismatches 0;
Qy 1 ANLWVTYYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTE 60
Db 33 ANLWVTYYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTE 92
Qy 61 NFNNKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 120
Db 93 NFNNKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 152
Qy 121 EQRKGEMRNCSEFNITTSIRDKVQREYALFKLDVEPIDDKNTNTNTKVLINCVTSVI 180
Db 153 EQRKGEMRNCSEFNITTSIRDKVQREYALFKLDVEPIDDKNTNTNTKVLINCVTSVI 212
Qy 181 TQACPVKVSPFPIPHYCTPTGTFALLKCKDKKFKNGTGTCTNVSTVQCTHGIRPVVSTQLLL 240
Db 213 TQACPVKVSPFPIPHYCTPTGTFALLKCKDKKFKNGTGTCTNVSTVQCTHGIRPVVSTQLLL 272
Qy 241 NGSLAEVEVIRSENFNNAKTIIVQLNVSEINCTFPNNHTRKRVTLGPRVWYTTGEI 300
Db 273 NGSLAEVEVIRSENFNNAKTIIVQLNVSEINCTFPNNHTRKRVTLGPRVWYTTGEI 332
Qy 301 LGNIROAHCNISRAQWNTLQQIATTLREQFGNKTIAPNOSGGDPEIVMHSFNCGEFF 360
Db 333 LGNIROAHCNISRAQWNTLQQIATTLREQFGNKTIAPNOSGGDPEIVMHSFNCGEFF 392

Qy 361 YCNSQTQFNSAWNVTSGTWSVTRKQDGTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 420
Db 393 YCNSQTQFNSAWNVTSGTWSVTRKQDGTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 452
Qy 421 LIRCSSNITGLLLTRDGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTKA 480
Db 453 LIRCSSNITGLLLTRDGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTKA 512
Qy 481 KRRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVQOONLLRAIK 540
Db 513 KRRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVQOONLLRAIK 572
Qy 541 AQHLLQLTWGIKQLOARILAVERYLKQDQLGFGCSGKLICTTAVPWNASNSKNTLD 600
Db 573 AQHLLQLTWGIKQLOARILAVERYLKQDQLGFGCSGKLICTTAVPWNASNSKNTLD 632
Qy 601 QIWNMTWMEWDREIDNTHLYTLIBESQOQEKNOQELLQDKWASL 649
Db 633 QIWNMTWMEWDREIDNTHLYTLIBESQOQEKNOQELLQDKWASL 681

RESULT 2
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties of
A;Reference number: A44001; MUID: 93021387; PMID: 1404605
A;Accession: H44001
A;Molecule type: DNA
A;Residues: 1-843 <LTY>
A;Cross-references: UNIPROT: P35961; UNIPARC: UPI000012A026; GB: M93258
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;19-35/Region: hydrophobic
F;30-489/Product: coat protein gp120 #status predicted <GP1>
F;490-843/Product: coat protein gp41 #status predicted <GP2>
F;499-515/Region: hydrophobic
F;673-689/Region: hydrophobic
F;738-755/Domain: transmembrane #status predicted <TMN>
F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 82.6%; Score 2869.5; DB 1; Length 843;
Best Local Similarity 83.5%; Pred. No. 1.5e-202;
Matches 541; Conservative 35; Mismatches 47; Indels 25; Gaps 6;
Qy 3 LWTVVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQEVLENTENF 62
Db 33 LWTVVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQEVLENTENF 92
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVLTNCTDLNNTNTNTTSELISIVVWEQ 122
Db 93 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVLTNCTDLNNTNTSSS---WET 146
Qy 123 RGKGEKNCNFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNVTITQ 182
Db 147 MERGEIKNCNFNITTSIRDKVQREYALFYNLVDVVID-----NASYRLISCNVTITQ 199
Qy 183 ACPKVSFEPPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGHIRPVVSTQLLNG 242
Db 200 ACPKVSFEPPIHYCAPAGFAILKCNDDKFKNGTGPCTNVSTVCTGHIRPVVSTQLLNG 259
Qy 243 SLAEEIVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWVYTTGILG 302

Db 260 SLAEEIVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKINIGPRALVTTGTBIIG 319
Qy 303 NIRAHCNISRACWNNTLOIATTLREQFG-NKTIAPNOSGGDPRIWHSFNCGGFFY 361
Db 320 DIRQAHCNLSKTQWENTLQIAIKLKEQFGNKTITIFNPSSGGDPRIWHSFNCGGFFY 379
Qy 362 CNSTQLFNSAWNVTSGTWSVTRKQDGTGDIITLPCRIKQIINRWQVVGKAMVALPIKGL 421
Db 380 CNSTQLF-----TWNDRKLNTGNITLPCRIKQIINRWQVVGKAMVALPIRQ 429
Qy 422 IRCSSNITGLLLTRDGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTKAK 481
Db 430 IRCSSNITGLLLTRDGGKDTNGTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTKAK 489
Qy 482 RRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVQOONLLRAIKA 541
Db 490 RRVQREKRAVG-LGALFLGFLGAAGSTWGAASITLTVOARQLLSGIVQOONLLRAIEA 548
Qy 542 QHLLQLTWGIKQLOARILAVERYLKQDQLGFGCSGKLICTTAVPWNASNSKNTLDQ 601
Db 549 QHLLQLTWGIKQLOARILAVERYLRDQLLGIWCSGKLICTTVPWNTSNKSLNE 608
Qy 602 IWNMTWMEWDREIDNTHLYTLIBESQOQEKNOQELLQDKWASL 649
Db 609 IWNMTWMEWDREIDNTHLYTLIBESQOQEKNEQELLQDKWASL 656

RESULT 3
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: A24774
R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.E.
Cell 45, 637-648, 1986
A;Title: Identification and characterization of conserved and variable regions in the env
A;Reference number: A24774; MUID: 86218077; PMID: 2423250
A;Accession: A24774
A;Molecule type: DNA
A;Residues: 1-856 <STA>
A;Cross-references: UNIPROT: P31872; UNIPARC: UPI000012A024; GB: M38432; NID: g19(c)
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-501/Product: coat protein gp120 #status predicted <GP1>
F;502-847/Product: coat protein gp41 #status predicted <GP2>
F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 82.3%; Score 2858; DB 1; Length 856;
Best Local Similarity 82.8%; Pred. No. 1.1e-201;
Matches 539; Conservative 34; Mismatches 60; Indels 18; Gaps 5;
Qy 3 LWTVVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQEVLENTENF 62
Db 33 LWTVVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQEVLENTENF 92
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVLTNCTDLNNTNTNTTSELISIVVWEQ 122
Db 93 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVLTNCTDLN-----ITDWN 140
Qy 123 R---GKGEKNCNFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNVTISV 179
Db 141 KTIIGGEKNCNFNITTSIRDKVQREYALFYKLDVVPVKSNNDSTYTRYLHCNVTISV 200
Qy 180 ITQACSKVSFEPPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGHIRPVVSTQLL 239
Db 201 ITQACSKVSFEPPIHYCAPAGFAILKCNDDKFKNGTGPCTNVSTVCTGHIRPVVSTQLL 260
Qy 240 LNSGLAEEVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWVYTTG 298

Db 261 LNSGLAEEIVIRSENFDTNAKTIIVHLNESVEINCTRPNNVRRHHIGPGAFY-TG 319
Qy 299 EILGNIRQAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 358
Db 320 EIRGNIRQAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 379
Qy 359 FFYCNSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPI 418
Db 380 FFYCNSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPI 438
Qy 419 KGLRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 478
Db 439 GGQIRCSNITGLLLTRDGGGSSREEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 498
Qy 479 KAKRVQREKRAVGMGLGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 499 KAKRVQREKRAVGMGLGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 558
Qy 539 IKAQOHLQLTVMGIGKQOARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKT 598
Db 559 IEAQOHLQLTVMGIGKQOARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKT 618
Qy 599 LDQIWNNTMWEDEIDNYTHLYTIEESQOQKNOQELLDKQWASL 649
Db 619 MDQIWNNTMWEDEIDNYTHLYTIEESQOQKNOQELLDKQWASL 669
RESULT 4
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI00010C516; EMBL:U63632; NID:gi1465777; PI
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
Query Match 82.0%; Score 2849.5; DB 2; Length 847;
Best Local Similarity 82.8%; Pred. No. 4.4e-201;
Matches 536; Conservative 40; Mismatches 52; Indels 19; Gaps 4;
Qy 3 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNTNTTIELSIIIVWEQ 122
Db 93 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNTNTTIELSIIIVWEQ 146
Qy 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 178
Db 147 -ERGEIKNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 200
Qy 183 ACPIKVSFEPIPIHYCTPTGPFALLKCNCKKFGNGTGPCTNVSTVQCTHGRPVVSTQL 242
Db 201 ACPIKVSFEPIPIHYCAPAGFALLKCNCKTNGKPCKNVSTVQCTHGRPVVSTQL 260
Qy 243 SLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 302
Db 261 SLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 320
Qy 303 NIROAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 362
Db 321 DIROAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 380

Qy 363 NSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPIKGLI 422
Db 381 NSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPIKGLI 434
Qy 423 RSCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPTAKR 482
Db 435 RSCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPTAKR 494
Qy 483 RVVQREKRAVGMGLGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAKQ 542
Db 495 RVVQREKRAVGMGLGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAKQ 553
Qy 543 QHLLQLTVMGIGKQOARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKTLDQI 602
Db 554 QHLLQLTVMGIGKQOARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKTLDQI 613
Qy 603 WNNMTMWEDEIDNYTHLYTIEESQOQKNOQELLDKQWASL 649
Db 614 WNNMTMWEDEIDNYTHLYTIEESQOQKNOQELLDKQWASL 660
RESULT 5
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in s
A:Reference number: Z17379; MUID:98178716; PMID:9519894
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: UNIPROT:O41883; UNIPARC:UPI00010B1F2; EMBL:U90934; NID:g2351783; PI
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
Query Match 81.7%; Score 2837; DB 2; Length 852;
Best Local Similarity 83.1%; Pred. No. 3.7e-200;
Matches 541; Conservative 35; Mismatches 53; Indels 22; Gaps 8;
Qy 3 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNTNTTIELSIIIVWEQ 122
Db 93 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNTNTTIELSIIIVWEQ 143
Qy 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 178
Db 144 NGGMEGEIKNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 198
Qy 179 VITQACPKVSFEPIPIHYCTPTGPFALLKCNCKKFGNGTGPCTNVSTVQCTHGRPVVSTQL 238
Db 199 VITQACPKVSFEPIPIHYCTPTGPFALLKCNCKKFGNGTGPCTNVSTVQCTHGRPVVSTQL 258
Qy 239 LLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 298
Db 259 LLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 318
Qy 299 EILGNIRQAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 358
Db 319 EILGNIRQAHCHNISRAQWNTLQOIATTLREPOGKNTIAFNQSSGGDPEIVMHSFNCGE 378
Qy 359 FFYCNSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPI 418
Db 379 FFYCNSTOLFNSANVTSNGTWSVTRKQDGTDIITLPCRKQIINRWQVGVKAMYPALPI 435
Qy 419 KGLRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 478

Db 436 RQIIRCSNITGILLTRDGGTNNSTNETFRPGGDMRDNWRSELYKYKVVKIEPLGVAPT 495
Qy 479 KAKRVVQREKRAVGMGLFGLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 496 KAKRVVQREKRAVG-IGALVFLGFLGAGSTMGAAVTLTVOARQLLSGIVQOQNLLRA 554
Qy 539 IKAQOHLQLTVMGIKOLQARILAVERYLKQDQLLGFPGWCGSKLICCTTAVPWNASWNSKT 598
Db 555 IEAQOHLQLTVMGIKOLQARVLAVERYLRDQQLLGIWCGSKLICCTTTPVWNASWNSKS 614
Qy 599 LDQIWNNTWMEWDREIDNTHLYTILIESQEQKXNQOELLQDLKWSL 649
Db 615 LDKIWNNTWMEWDREIDNTHLYTILIESQEQKXNQOELLQDLKWSL 665

RESULT 6
S13289
env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13289
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A;Reference number: S13288; MUID:91043044; PMID:2172833
A;Accession: S13289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-847 <OR>
A;Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C;Superfamily: type E retrovirus env polyprotein

Query Match 81.6%; Score 2836.5; DB 2; Length 847;
Best Local Similarity 82.5%; Pred. No. 4e-200;
Matches 534; Conservative 39; Mismatches 55; Indels 19; Gaps 4;

Qy 3 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVLENTENF 62
Db 33 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVLENTENF 92
Qy 63 NMKNVQEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSELIIIVWEQ 122
Db 93 NMKNVQEQMHEDIISLWQSLKPCVKLTPLCVTLNCKDVNATNTINDSEGTM----- 146
Qy 123 RGKEMRCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYRLINCNTSVITQ 182
Db 147 -ERGEIKNCFSNITTSIRDEVQREYALFYKLDVVPIDN-----NNTSYRLISCDTSVITQ 200
Qy 183 ACPKVSPEPIPIHYCTPTGPFALLKCKDKKFGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 201 ACPKISPEPIPIHYCAPAGFAILKCKDKTNGKPGCKNVSTVQCTHGIRPVVSTQLLNG 260
Qy 243 SLAEVEVIRSENFNTNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWVTTGILG 302
Db 261 SLAEVEVIRSENFNTNAKTIIVQLKESVINECTRPNNHTRKSIHIGPGRAFVTTGIIIG 320
Qy 303 NIROAHCHNISRAQNNLTLOQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGFFYC 362
Db 321 DIRQACHNISRAKWNLTLOQIVIKLREQFNKTIIVFNHSSGGDPEIVMHSFNCGGFFYC 380
Qy 363 NSTOLENSANVTNSGTWSTVRKQKQDGIITLPCRKQIINRWQVVGKAMYPALPIKGLI 422
Db 381 NSTQLNNSTWNNNTGFS-----NNTGNTITLPCRKQIINRWQVVGKAMYPALPIKGLI 434
Qy 423 RCSSNITGLLLTRDGGGENOTTBIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPTAKR 482
Db 435 RCSSNITGLLLTRDGGGENOTTBIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPTAKR 494
Qy 483 RVVQREKRAVGMGLFGLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRAIKAQ 542
Db 495 RVVQREKRAVG-IGAVFLGFLGAGSTMGAAVTLTVOARQLLSGIVQOQNLLRAIEAQ 553

Qy 543 QHLLQLTVMGIKOLQARILAVERYLKQDQLLGFPGWCGSKLICCTTAVPWNASWNSKTLDQI 602
Db 554 QRMQLTVMGIKOLQARVLAVERYLRDQQLLGIWCGSKLICCTTAVPWNASWNSKSLDRI 613
Qy 603 WNNMTWMEWDREIDNTHLYTILIESQEQKXNQOELLQDLKWSL 649
Db 614 WNNMTWMEWDREIDNTHLYTILIESQEQKXNQOELLQDLKWSL 660

RESULT 7
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: A31667
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A;Reference number: A94389; MUID:89085613; PMID:2789516
A;Accession: A31667
A;Molecule type: DNA
A;Residues: 1-852 <ANA>
A;Cross-references: UNIPROT:P12488; UNIPARC:UPI0000174A36
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F;1-516/Product: coat protein gp120 #status predicted <CP1>
F;517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 81.1%; Score 2816.5; DB 1; Length 852;
Best Local Similarity 80.8%; Pred. No. 1.2e-198;
Matches 528; Conservative 53; Mismatches 43; Indels 31; Gaps 7;

Qy 3 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVLENTENF 62
Db 34 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVLENTENF 93
Qy 63 NMKNVQEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSELIIIVWEQ 122
Db 94 NMKNVQEQMHEDIISLWQSLKPCVKLTPLCVTLNCHDFNATNATNS----- 143
Qy 123 RGK-----GEMRCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYRLINCNTS 178
Db 144 -GOMEEGEMKCSFNITTSIRDKMQREYALFYKLDVDPIDNDK---TNTRYRLISCNTS 199
Qy 179 VITQACPVSFPEPIPIHYCTPTGPFALLKCKDKKFGTGPCTNVSTVQCTHGIRPVVSTQL 238
Db 200 VITQACPVTPEPIPIHYCAPAGFAILKCKNKKFGTGPCTNVSTVQCTHGIRPVVSTQL 259
Qy 239 LINGSLAEEVIRSENFNTNAKTIIVQLNVSVINECTRPNNHTRKRVTLGPRVWVTTG 298
Db 260 LINGSLAEEVIRSENFNTNVKTIIVQLNESVINECTRPNNHTRKRTIWTGPRVVTG 319
Qy 299 EILGNIRQACHNISRAQNNLTLOQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGE 358
Db 320 QIIGDIRRAHCHLSRSKWNLTLOQIVTKLRVQFNKTIIVFNRSRSGGDPPEIVMHSFNCGGE 379
Qy 359 FFYCNSTQLPNSAW--NVTSNGTWSTVRKQKQDGIITLPCRKQIINRWQVVGKAMYPAL 416
Db 380 FFCNTQQLPNSWTYRNTGNIT-----EGNSPITLPCRKQIINRWQVVGKAMYPAL 431
Qy 417 PIKGLIRCSNITGLLLTRDGGGENOT--TEIFRPGGDMRDNWRSELYKYKVKVIEPLG 474
Db 432 PIRGQIKCSSNITGLLLTRDGGNNNETTDTFIRPGGDMRDNWRSELYKYKVKVIEPLG 491
Qy 475 VAPTAKRVVQREKRAVGMGLFGLGAGSTMGATSMALTVOARQLLSGIVQOQN 534
Db 492 VAPTAKRVVQREKRAVG-LGALFLGFLGAGSTMGAAVTLTVOARQLLSGIVQOQN 550
Qy 535 LLRAIKAQOHLQLTVMGIKOLQARILAVERYLKQDQLLGFPGWCGSKLICCTTAVPWNASW 594

551 LMAIEAQOQHLELTVVNGIKQLQARVLAVERYLKQDOLLGIMGSGKLICTTAVPWNASW 610

595 SNKTLDOIWNNTWMEWDREIDNTYTHLYTILIESQKQEKNOQLLQLDKWSL 649

611 SNKSLSDIWDNMTWMEWEREIDNTYTHLYSIEDSQIQEKNKELLELDKWSL 665

RESULT 8

VCLJAZ2

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <SNA>

A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:g328658; PIDN:

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458

F:610,624,636,815/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 81.0%; Score 2815.5; DB 1; Length 855;

Best Local Similarity 81.2%; Pred. No. 1.4e-198;

Matches 528; Conservative 47; Mismatches 58; Indels 17; Gaps 6;

3 LWVTYVYGVVPWKGAATTTLCASDAKAYDTEAHNVWATHACVPTNPNQBVLENTEFN 62

33 LWVTYVYGVVPWKGAATTTLCASDARAYDTEAHNVWATHACVPTDNPQBVLENTEFN 92

63 NMWKNMVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNTNTNTTTELSIIVVWEQ 122

93 NMWKNMVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLGKATNTSSN-----WKE 146

123 RGKGMENCSFNITTSIRDQVREYALFYKLDVEPIDDNKNNTNTKYRLINCNTSVITQ 182

147 EIKGEIKNCSFNITTSIRDKIQENALFRNLDVVPIDNASTTTNTYNTYRLIHCNRSVITQ 206

183 ACPKVSPEPIPIHYCTPTGALLKCNDDKKNFGPGCTNVSTVCTGTHGIRVPVSTOLLNG 242

207 ACPKVSPEPIPIHYCTPTAGFAILKCNKNTFNGKPGCTNVSTVCTGTHGIRVINSTOLLNG 266

243 SLAEEVVIRSENFNTNAKTIIVQLNVSVSEINCTRPNNHTRKRVTLGPGRWVTTTGEILG 302

267 SLAEEVVIRSENFNTNAKTIIVQLNESVAINCTRPNNHTRKSIYIGPGRAFHTTGRILG 326

303 NIROAHNCNISRAQNNNTLQIATTLREQFG-NKTIAFNQSGGDPPEIVMHSFNCGGEFFY 361*

327 DIRAHNCNISRAQNNNTLEQIVKKLREQFGNNKTIIVFNQSGGDPPEIVMHSFNCRGEFFY 386

362 CNSTOLFNSAENVVT-SNGTWSVTRKQDGTGDIITLPCRIKOIINRWQVVKAMVALPIKG 420

387 CNTTQLFNNTWRLNHLTGST-----KGNDT---IILPCRIKOIINMWQEVGKAMYPPIGG 438

421 LIRCSNITGLLLTRDGG-GENOTTEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPTK 479

439 QISCSNITGLLLTRDGGTVNDTVEFRPGGDMRDNRWSELYKYKVKIEPLGIAPTK 498

480 AKRIVQREKRAVGMGLGAMFLGFIAGAGSTVGATSMALTVOARQLLSGIVQOQNLLRAI 539

499 AKRIVQREKRAVIGVAMFLGFIAGAGSTVGAVSLTVOARQLLSGIVQOQNLLRAI 558

[illegible]

RESULT 10
VCLJXJ

env polypeptin precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N;Alternate names: coat polypeptin
N;Contains: coat protein gp120; coat protein gp32
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C;Accession: B42995
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A;Reference number: A42995; MUID:92351552; PMID:1322587
A;Accession: B42995
A;Molecule type: mRNA
A;Residues: 1-729 <SHI>
A;Cross-references: UNIPARC:UPI000174A37; GB:S41266; GB:D01206
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polypeptin
C;Keywords: coat protein; glycoprotein; polypeptin; transmembrane protein
F;1-689/Domain: extracellular #status predicted <EXT>
F;1-33/Domain: signal sequence #status predicted <SIG>
F;17-33/Region: hydrophobic #status predicted
F;34-517/Product: coat protein gp120 #status predicted <CP1>
F;514-517/Region: cleavage processing #status predicted
F;518-729/Product: coat protein gp32 #status predicted <CP2>
F;518-534/Region: hydrophobic #status predicted
F;690-711/Domain: transmembrane #status predicted <TM>
F;712-729/Domain: intracellular #status predicted <INT>
F;93, 141, 145, 146, 163, 191, 192, 237, 241, 248, 269, 283, 296, 308, 338, 345, 361, 367, 397, 403, 408, 414

Query Match 80.8%; Score 2808; DB 1; Length 729;
Best Local Similarity 81.8%; Pred. No. 4e-198;
Matches 534; Conservative 49; Mismatches 48; Indels 22; Gaps 9;

QY	3	LWTVYGVVPEKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNQVWLENTEF	62
DB	39	LWTVYGVVPEKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPNQVWLENTEF	98
QY	63	NMWKNNVQWHEHDIISLWQSLKPCVKLTPLCVLTNCTDLNNTNTTTELSIIVVWEQ	122
DB	99	NMWKNNVQWHEHDIISLWQSLKPCVKLTPLCVLTNCTDLNNTNTTTELSIIVVWEQ	151
QY	123	RGKGEWNCFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTKYRLINCNTSVITQ	182
DB	152	KMKGEIKNCNFVNTIRDKVQREYALFYKLDVVPIDNNDNST-NTCYRLISCDTSVITQ	210
QY	183	ACPVSPEPIPIHYCTPTGALLKCNCKKNGTGPCTNVTQCTHGIRPWSVSTOLLNG	242
DB	211	ACPVSPEPIPIHYCTPTGALLKCNCKNTFTNGTGPCKNVSTVQCTHGIRPWSVSTOLLNG	270
QY	243	SLAEVEVIRSENFPTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRWVYTTGELLG	302
DB	271	SLAEGVVIRSENFPTNNAKTIIVQLNETVKINCIRPNKTRKRVTLGPGRWVYTTGELLG	330
QY	303	NIQRAHCNISRAQWNTLQOIATTLREQNGKTIAFNQSGGDPPEIVMHSFNCGGFFVYC	362
DB	331	DIRQAHCNISRAEWNTLEQIANKLKQFENKTIIVFNQSGGDPPEIVMHSFNCGGFFVYC	390
QY	363	NSTOLFSAWNTVSGTWSTVTRKQKTG-DIITLPCRKQIINRWQVGVKMYALDIKGL	421
DB	391	DSSQLFNSTH--LSNGTW-----WNGTGPENITLPCRKQIIVNMQEVGKMYAPPIRGQ	443
QY	422	IRCSSNITGLLLTRDGG-----GENQTETLFRPGGDMRDNRSELYKVKVXIEPLGVA	476
DB	444	IRCSSNITGLLLTRDGGTQNNNTSSIEIFRPGGDMRDNRSELYKVKVXIEPLGVA	503
QY	477	PTAKRVVQREKAVGMLGAMFLGFLGAAGSTGATSMALTVOARQLLSGIVQOQNLL	536
DB	504	PTAKRVVQREKAVG-IGAVFLGFLGAAGSTGAAVTLTVQARQLLPVIGVQOQNLL	562

Qy	537	RAIKAOQHLLQLTWGIKQLOARILAVERYLKQDOQLLGFWGCSGKLICTTAVPWNASWSN	536
Db	563	RAIDAOQHLLQLTWGIKQLOARVLAVERYLKQDOQLMGWGCSGKFICTTAVPWNTSWSN	622
Qy	597	KTLDQIOWNNMTWMEWDREIDNYTHLYVTLIESNQOEKKNQOELLQDKWASL	649
Db	623	KSFNEIWDNMTWMEWEREINNYTNLYNLTIESNQOEKNEQDLDLADKWSL	675
<p>RESULT 11</p> <p>VCLJKB</p> <p>env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-1-gp1-gp2)</p> <p>N:Alternate names: coat polypeptide</p> <p>N:Contains: coat protein gp120; coat protein gp41</p> <p>C:Species: human immunodeficiency virus type 1, HIV-1</p> <p>A:Note: host Homo sapiens (man)</p> <p>C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004</p> <p>C:Accession: A42995</p> <p>F:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T. Virology 189, 534-546, 1992</p> <p>A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated gag gene</p> <p>A:Reference number: A42995; MUID:923351552; PMID:1322587</p> <p>A:Accession: A42995</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-861 <SHI></p> <p>A:Cross-references: UNIPROT:P31819; UNIPARC:UPI000012A019; GB:S41266; GB:D01206</p> <p>C:Genetics:</p> <p>A:Gene: env</p> <p>C:Superfamily: type E retrovirus env polypeptide</p> <p>C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein</p> <p>F:1-689/Domain: extracellular #status predicted <EXT></p> <p>F:1-33/Domain: signal sequence #status predicted <SIG></p> <p>F:17-33/Region: hydrophobic #status predicted</p> <p>F:34-517/Product: coat protein gp120 #status predicted <CP1></p> <p>F:514-517/Region: cleavage processing #status predicted</p> <p>F:518-861/Product: coat protein gp41 #status predicted <CP2></p> <p>F:518-534/Region: hydrophobic #status predicted</p> <p>F:690-711/Domain: transmembrane #status predicted <TM1></p> <p>F:712-861/Domain: intracellular #status predicted <INT></p> <p>F:756-772/Region: hydrophobic #status predicted</p> <p>F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,1108,1109,1110,1111,1112,1113,1114,1115,1116,1117,1118,1119,1120,1121,1122,1123,1124,1125,</p>			

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QY 422 IRCSSNITGLLLTRDGG-----GENQTEIFRPGGDMRDNRSELYKYKVKIEPLGVA 476
D 444 IRCSSNITGLLLTRDGGTQNNNTSSIEIFRPGGDMRDNRSELYKYKVKIEPLGVA 503
QY 477 PTKARRVQREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLL 536
D 504 PTKARRVQREKRAVG-IGAVFLGFLGAAGSTMGAAVLTVOARQLLSGIVQOQNLL 562
QY 537 RAIKAQHLLQLTVWGIKQARILAVERYLKQDQLLGFMGCSGKLCITTAVPNWSN 596
D 563 RAIDQAQHLLQLTVWGIKQARILAVERYLKQDQLLGFMGCSGKLCITTAVPNWSN 622
QY 597 KTLDOIWNMTWMDREIDNYTHLYTLIESQOQEKQOELLQDLKWSL 649
D 623 KSFNEIWNMTWMDREINNYTHLYTLIESQOQEKQOELLQDLKWSL 675

RESULT 12
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora-
nberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
A;Accession: A03973
A;Molecule type: DNA
A;Residues: 1-856 <RAT>
A;Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;86,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 80.8%; Score 2806.5; DB 1; Length 856;
Best Local Similarity 82.8%; Pred. No. 6.4e-198;
Matches 539; Conservative 35; Mismatches 58; Indels 19; Gaps 9;
QY 3 LWTVYVGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENTVF 62
D 34 LWTVYVGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTDPPQEVVLENTVF 93
QY 63 NMWKNVQVQHEHDIISLDQSLKPCVKLPLCVLTNCTDLNTNTNTTSLSIIVVWEQ 122
D 94 NMWKNVQVQHEHDIISLDQSLKPCVKLPLCVLSKCTDL--KNDNTNNTSSSGRIME- 150
QY 123 RGKEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNVTIQ 182
D 151 --KGEIKNCSFNISTSRGKQVEYAFYKLDIIPIDN-----DTSYTLTSCNVTIQ 203
QY 183 ACPKVSFEPIPIHYCTPTGALLKCNCKENGTCPTNVTSTVQCTHGRIPVWSTQLLNG 242
D 204 ACPKVSFEPIPIHYCAPAGFALLKCNKNTNGTCPTNVTSTVQCTHGRIPVWSTQLLNG 263
QY 243 SLAEVWIRSENFTNNAKTIIVQLNVSVINCTRNPNHTRK--RVTLGPRGVYTTGEI 300
D 264 SLAEVWIRSANFTDNAKTIIVQLNQSVINCTRNPNHTRKSIIRQGRGPAFTIGKI 323
QY 301 LGNIROAHNISRAQWNTLQOIATTLREQFG-NKTIAPNQSSGGDPEIWMHFNCCGEF 359
D 324 -GNMROAHNISRAKWNNTLKQIDSLREQFGNNKTIIPKQSSGGDPEIWMHFNCCGEF 382
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QY 360 FYCNSSTOLNSANNVTSGTWSVTRKQKDTG-DIITLPCRIKQIINRVOVVGKAMYALPI 418
D 383 FYCNSSTOLNSFW---FNSWTSGKSNNTGSETITLPCRIKQIINRVOVVGKAMYAPPI 439
QY 419 KGLIRCSSNITGLLLTRDGGENQTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
D 440 SGOIRCSSNITGLLLTRDGGNNSESEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 499
QY 479 KAKRRVVQREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
D 500 KAKRRVVQREKRAVG-IGALFLGFLGAAGSTMGAASTMLTVOARQLLSGIVQOQNLLRA 558
QY 539 IKAQHLLQLTVWGIKQARILAVERYLKQDQLLGFMGCSGKLCITTAVPNWSNKT 598
D 559 IEAQHLLQLTVWGIKQARILAVERYLKQDQLLGFMGCSGKLCITTAVPNWSNKS 618
QY 599 LDOIWNMTWMDREIDNYTHLYTLIESQOQEKQOELLQDLKWSL 649
D 619 LEQIWNMTWMDREINNYTHLYTLIESQOQEKQOELLQDLKWSL 669

RESULT 13
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03974
R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retroviral
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03974
A;Molecule type: DNA
A;Residues: 1-856 <MUE>
A;Cross-references: UNIPROT:P03376; UNIPARC:UPI000012A01F; GB:K02083; NID:9555008; PIDN:
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;86,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 80.8%; Score 2799.5; DB 1; Length 856;
Best Local Similarity 82.5%; Pred. No. 2.1e-197;
Matches 537; Conservative 36; Mismatches 59; Indels 19; Gaps 9;
QY 3 LWTVYVGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENTVF 62
D 34 LWTVYVGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTDPPQEVVLENTVF 93
QY 63 NMWKNVQVQHEHDIISLDQSLKPCVKLPLCVLTNCTDLNTNTNTTSLSIIVVWEQ 122
D 94 NMWKNVQVQHEHDIISLDQSLKPCVKLPLCVLSKCTDL--KNDNTNNTSSSGRIME- 150
QY 123 RGKEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNVTIQ 182
D 151 --KGEIKNCSFNISTSRGKQVEYAFYKLDIIPIDN-----DTSYTLTSCNVTIQ 203
QY 183 ACPKVSFEPIPIHYCTPTGALLKCNCKENGTCPTNVTSTVQCTHGRIPVWSTQLLNG 242
D 204 ACPKVSFEPIPIHYCAPAGFALLKCNKNTNGTCPTNVTSTVQCTHGRIPVWSTQLLNG 263
QY 243 SLAEVWIRSENFTNNAKTIIVQLNVSVINCTRNPNHTRK--RVTLGPRGVYTTGEI 300
D 264 SLAEVWIRSANFTDNAKTIIVQLNQSVINCTRNPNHTRKSIIRQGRGPAFTIGKI 323
QY 301 LGNIROAHNISRAQWNTLQOIATTLREQFG-NKTIAPNQSSGGDPEIWMHFNCCGEF 359
D 324 -GNMROAHNISRAKWNNTLKQIDSLREQFGNNKTIIPKQSSGGDPEIWMHFNCCGEF 382
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Db 324 -GNNRQAHCHNISRAKWNNTLQKIDSKLREQFGNKKTIIFKQSSGGDPPEIVTHSFNCGGF 382
QY 360 FYCNSLTQFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKQIOLINRWQVVGKAMVALPI 418
Db 383 FYCNSLTQFNSW---FNSWTSGSNTSGSDTITLPCRKQIOLINRWQVVGKAMVALPI 439
QY 419 KGLIRCSNITGLLLTRDGGGQNTTEIFRPGGDMRDNRSELYKYKVKIPLGVP 478
Db 440 SGQIRCSNITGLLLTRDGGGNNNESEIFRPGGDMRDNRSELYKYKVKIPLGVP 499
QY 479 KAKRRVVRQEKRAVGMFLGAGTGAAGTGAATGATSMALTVQARQLLSGIVQOQNLLRA 538
Db 500 KAKRRVVRQEKRAVG-IGALFLGAGTGAAGTGAATGATSMALTVQARQLLSGIVQOQNLLRA 558
QY 539 IKAQOHLQLTVMGIKQARILAVERYLKDQQLLFGWCGSGKLICTTAVPWNASNKT 598
Db 559 IEAQOHLQLTVMGIKQARILAVERYLKDQQLLFGWCGSGKLICTTAVPWNASNKS 618
QY 599 LDQIWNMTWMDREIDNTHLYTLIESQOQEKNOQELLQLOKWSL 649
Db 619 LEQIWNMTWMDREINNTYLSLHSLIESQOQEKNEQELLELDKWSL 669

RESULT 14
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03975
R;Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:K02013; NID:G326417; PIDN:
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 80.5%; Score 2795; DB 1; Length 861;
Best Local Similarity 82.4%; Pred. No. 4.5e-197;
Matches 539; Conservative 37; Mismatches 58; Indels 20; Gaps 10;

QY 3 LWTVYVYGVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLNVTENF 62
Db 34 LWTVYVYGVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLNVTENF 93

QY 63 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLN--TN--NTNTTTELSIIV 119
Db 94 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVSLKCTDLNATNTNNTSSSGEMM 153

QY 120 WEQRGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCTSV 179
Db 154 ME---KGEIKNCFSNISTSRGKQVEYAFYKLDIIPIDN-----DTSYLTSCNTSV 205

QY 180 ITQACPKVSEPIPIHYCTPTGFALLKCNCKFKENGPGCTNVTSTVQCTHGIRPVSTQLL 239
Db 206 ITQACPKVSEPIPIHYCAPAGFALLKCNCKTNGTNGTNGTNGTNGTNGTNGTNGTNGT 265

QY 240 LNSLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRK--RVTLGGRVWYTT 297
Db 266 LNSLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKSIQRGPGRAFVTI 325

QY 298 GEILGNIRQAHCHNISRAQWNNTLQIATTLREQFG-NKTIAFNQSSGGDPPEIVHMSFNCG 356
Db 326 GKI-GNNRQAHCHNISRAKWNNTLQIASKLREQFGNKKTIIFKQSSGGDPPEIVTHSFNCG 384
QY 357 GBFFFCNSLTQFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKQIOLINRWQVVGKAMVA 415
Db 385 GBFFFCNSLTQFNSW---FNSWTSGSNTSGSDTITLPCRKQIOLINRWQVVGKAMVA 441
QY 416 LPIKGLIRCSNITGLLLTRDGGGQNTTEIFRPGGDMRDNRSELYKYKVKIPLGVP 475
Db 442 PPISSGQIRCSNITGLLLTRDGGGNNNGSEIFRPGGDMRDNRSELYKYKVKIPLGVP 501
QY 476 APTKAKRRVVRQEKRAVGMFLGAGTGAAGTGAATGATSMALTVQARQLLSGIVQOQNLL 535
Db 502 APTKAKRRVVRQEKRAVG-IGALFLGAGTGAAGTGAATGATSMALTVQARQLLSGIVQOQNLL 560
QY 536 LRAIKAAQOHLQLTVMGIKQARILAVERYLKDQQLLFGWCGSGKLICTTAVPWNASWS 595
Db 561 LRAIEAQOHLQLTVMGIKQARILAVERYLKDQQLLFGWCGSGKLICTTAVPWNASWS 620
QY 596 NKTLDQIWNMTWMDREIDNTHLYTLIESQOQEKNOQELLQLOKWSL 649
Db 621 NKSLEQIWNMTWMDREINNTYLSLHSLIESQOQEKNEQELLELDKWSL 674

RESULT 15
S33985
env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <CAR>
A;Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:G60192; PIDN:
C;Superfamily: type E retrovirus env polyprotein

Query Match 80.1%; Score 2782; DB 2; Length 851;
Best Local Similarity 82.0%; Pred. No. 4e-196;
Matches 534; Conservative 39; Mismatches 54; Indels 24; Gaps 9;

QY 3 LWTVYVYGVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLNVTENF 62
Db 34 LWTVYVYGVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLNVTENF 93

QY 63 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVVWEQ 122
Db 94 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVSLKCTDL--KNDTNTNNTSSSGRIME- 150

QY 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCTSVITQ 182
Db 151 --KGEIKNCFSNISTSRGKQVEYAFYKLDIIPIDN-----DTSYLTSCNTSVITQ 203

QY 183 ACPKVSFEPIPIHYCTPTGFALLKCNCKFKENGPGCTNVTSTVQCTHGIRPVVSTQLLNG 242
Db 204 ACPKVSFEPIPIHYCAPAGFALLKCNCKTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 263

QY 243 SLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKVTL--GPGRVWYTTGEI 300
Db 264 SLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKIRQIRGPGRAFVTIGKI 323

QY 301 LGNIRQAHCHNISRAQWNNTLQIATTLREQFG-NKTIAFNQSSGGDPPEIVHMSFNCGGBF 359
Db 324 -GNNRQAHCHNISRAKWNNTLQIASKLREQFGNKKTIIFKQSSGGDPPEIVTHSFNCGGBF 382

QY 360 FYCNSLTQFNSAWNVT--SNGTWSVTRKQKDTGDIITLPCRKQIOLINRWQVVGKAMVALPI 418
Db 383 FYCNSLTQFNSWSTWSTGSGNNT-----EGSDTITLPCRKQIOLINRWQVVGKAMVALPI 434

Qy 419 KGLRCSNITGLLLTRDGGGNOTTEIFRPGGDMRDNRSELYKYKVXKIEPLGVAPT 478
Db :|||||
Qy 435 SGQIRCSNITGLLLTRDGGNSNESEIFRPGGDMRDNRSELYKYKVXKIEPLGVAPT 494
Db :|||||
Qy 479 KAKRRVVQREKRAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQQNNLLRA 538
Db :|||||
Qy 495 KAKRRVVQREKRAVG-IGALFLGFLGAGSTMGAAASMTLTVOARQLLSGIVQQQNNLLRA 553
Db :|||||
Qy 539 IKAQOHLLOLTWGIKQLOARILAVERYLKQOQLLGFWGCSGKLICTTAVPWNASWSNKT 598
Db :|||||
Qy 554 IEAQOHLLOLTWGIKQLOARILAVERYLKQOQLLGFWGCSGKPICTTAVPWNASWSNKS 613
Db :|||||
Qy 599 LDOJWNMTWMEWDREIDNYTHLYTLIEESQNOEKNOQELLOLDKWASL 649
Db :|||||
Qy 614 LEQIWNMTWMEWDREINNYTSLIHSLEESQNOEKNEQELLEDKWASL 664
Db :|||||

Search completed: March 7, 2006, 17:51:34
Job time : 51.7758 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:55 ; Search time 297.698 Seconds
(without alignments)
1538.097 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474
Sequence: 1 ANLWVTYYGVVWKEATTT.....ONQOEKNQQLQDKWASL 649

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

*Med. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3474	100.0	868	1 ENV_HVIC4	P05879 human immun
2	2927	84.3	854	2 Q7SVL3_9HIV1	Q7svl3 human immun
3	2908	83.7	854	2 O40222_9HIV1	O40222 human immun
4	2906.5	83.7	853	2 O6UYR2_9HIV1	O6uyr2 human immun
5	2905	83.6	860	2 Q7SVL7_9HIV1	Q7svl7 human immun
6	2900.5	83.5	863	2 Q6UYPO_9HIV1	Q6uypo human immun
7	2899	83.4	852	2 Q7SVL5_9HIV1	Q7svl5 human immun
8	2898.5	83.4	869	2 Q6UYM7_9HIV1	Q6uym7 human immun
9	2896.5	83.4	853	2 Q03811_9HIV1	Q03811 human immun
10	2896.5	83.4	863	2 Q6UYN7_9HIV1	Q6uyn7 human immun
11	2895	83.3	850	2 Q7SVL4_9HIV1	Q7svl4 human immun
12	2893.5	83.3	861	2 Q7SVU4_9HIV1	Q7svu4 human immun
13	2892.5	83.3	867	2 Q6UYPI_9HIV1	Q6uypi human immun
14	2890.5	83.2	851	2 Q52S58_9HIV1	Q52s58 human immun
15	2889.5	83.2	865	2 Q6UYN6_9HIV1	Q6uyn6 human immun
16	2889	83.2	841	2 Q9QKJ1_9HIV1	Q9qkj1 human immun
17	2889	83.2	849	2 Q6UYQ5_9HIV1	Q6uyq5 human immun
18	2889	83.2	862	2 Q7SVU5_9HIV1	Q7svu5 human immun
19	2888.5	83.1	853	2 Q6UYR3_9HIV1	Q6uyr3 human immun
20	2888	83.1	862	2 Q7SVU1_9HIV1	Q7svu1 human immun
21	2887.5	83.1	853	2 Q6UZ37_9HIV1	Q6uz37 human immun
22	2887.5	83.1	861	2 Q7SVI0_9HIV1	Q7svi0 human immun
23	2885.5	83.1	850	2 Q6UYQ1_9HIV1	Q6uyq1 human immun
24	2885.5	83.1	851	2 Q6UZ40_9HIV1	Q6uz40 human immun
25	2885.5	83.1	854	2 Q6TAN8_9HIV1	Q6tan8 human immun
26	2885	83.0	872	2 Q6UYN9_9HIV1	Q6uyn9 human immun
27	2884.5	83.0	851	2 Q6UYR5_9HIV1	Q6uyr5 human immun
28	2884	83.0	852	2 Q6UZ34_9HIV1	Q6uz34 human immun
29	2883.5	83.0	847	1 ENV_HVIS1	P19550 human immun
30	2883.5	83.0	861	2 Q7SVU0_9HIV1	Q7svu0 human immun
31	2883	83.0	862	2 Q7SVU0_9HIV1	Q7svu0 human immun

32	2883	83.0	862	2 Q7SVU3_9HIV1	Q7svu3 human immun
33	2883	83.0	868	2 Q6UYM9_9HIV1	Q6uym9 human immun
34	2881	82.9	866	2 Q6UYN8_9HIV1	Q6uyn8 human immun
35	2880.5	82.9	851	2 Q6UYR7_9HIV1	Q6uyr7 human immun
36	2879.5	82.9	849	2 Q6UYR9_9HIV1	Q6uyr9 human immun
37	2879.5	82.9	861	2 Q7SVJ8_9HIV1	Q7svj8 human immun
38	2879.5	82.9	861	2 Q7SVU6_9HIV1	Q7svu6 human immun
39	2879.5	82.9	861	2 Q7SVU8_9HIV1	Q7svu8 human immun
40	2878.5	82.9	854	2 Q6TAN5_9HIV1	Q6tan5 human immun
41	2877.5	82.8	847	2 Q6BC04_9HIV1	Q6bc04 human immun
42	2876.5	82.8	854	2 Q6TAN7_9HIV1	Q6tan7 human immun
43	2876	82.8	864	2 Q6UYN4_9HIV1	Q6uyn4 human immun
44	2875	82.8	854	2 Q6UZ36_9HIV1	Q6uz36 human immun
45	2874	82.7	850	2 Q6UYQ8_9HIV1	Q6uyq8 human immun

ALIGNMENTS

RESULT 1

ID	ENV_HVIC4	STANDARD	PRT	868 AA
AC	P05879;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	Glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	Name=ENV;			
OS	Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).			
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;			
OC	Lentivirus; Primate lentivirus group.			
OX	NCBI_TaxID=11687;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=87041461; PubMed=3490666;			
RA	Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,			
RA	Andersen P.R., Devare S.G.;			
RT	"Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).			
RL	[2]			
RN	PROTEIN SEQUENCE OF 34-43.			
RP	MEDLINE=90253924; PubMed=2187500;			
RX	Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,			
RA	Devico A.L., Copeland T., Oroszian S., Gallo R.C., Sargadharan M.G.;			
RT	"Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1."			
RL	AIDS Res. Hum. Retroviruses 6:371-380 (1990).			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-----			
CC	EMBL: M13137; AAA44311.1; -; Genomic_RNA.			
DR	PIR: C25523; VCLJH4.			
DR	HSPSP: P19549; INEQ.			
DR	SMR: P05879; 84-128, 87-212, 206-503, 552-638.			
DR	HIV: M13137; ENV\$CDC45.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
DR	AIDS; Capsid protein; Direct protein sequencing; Glycoprotein; Polyprotein; Signal; Structural protein; Transmembrane.			
FT	SIGNAL 1 33			
FT	CHAIN 34 522			Exterior membrane glycoprotein.
FT	CHAIN 523 868			Transmembrane glycoprotein.
FT	CARBOHYD 89 89			N-linked (GlcNAc. . .) (potential).
FT	CARBOHYD 131 131			N-linked (GlcNAc. . .) (potential).

FT	CARBOHYD	138	138	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	139	139	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	142	142	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	162	162	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	166	166	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	195	195	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	198	198	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	208	208	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	245	245	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	252	252	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	273	273	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	287	287	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	300	300	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	306	306	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	312	312	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	342	342	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	349	349	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	365	365	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	371	371	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	395	395	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	405	405	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	409	409	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	459	459	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	473	473	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	623	623	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	628	628	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	637	637	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	649	649	N-linked	(GlcNAc. . .)	(Potential).
FT	CARBOHYD	828	828	N-linked	(GlcNAc. . .)	(Potential).
FT	DISULFID	55	75	By similarity.		
FT	DISULFID	120	216	By similarity.		
FT	DISULFID	127	207	By similarity.		
FT	DISULFID	132	163	By similarity.		
FT	DISULFID	229	258	By similarity.		
FT	DISULFID	239	250	By similarity.		
FT	DISULFID	307	341	By similarity.		
FT	DISULFID	387	456	By similarity.		
FT	DISULFID	394	429	By similarity.		
SQ	SEQUENCE	868 AA;	98699 MW;	Al1527FC52A6F0C8	CRC64;	
Query Match						
Best Local Similarity 100.0%; Score 3474; DB 1; Length 868;						
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	ANLWTVYGVVYGVVKEATTTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE	60			
DB	33	ANLWTVYGVVYGVVKEATTTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE	92			
QY	61	NFMNKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSLIIVVW	120			
DB	93	NFMNKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSLIIVVW	152			
QY	121	EQKGEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNKTNTKYRLINCNTSVI	180			
DB	153	EQKGEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNKTNTKYRLINCNTSVI	212			
QY	181	TOACPVKSEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL	240			
DB	213	TOACPVKSEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL	272			
QY	241	NGSLAEEVVIRSENFNTNNAKTIIVQLNVSVENCTRPNNHTRKRVTLGPGRVVYTTGEI	300			
DB	273	NGSLAEEVVIRSENFNTNNAKTIIVQLNVSVENCTRPNNHTRKRVTLGPGRVVYTTGEI	332			
QY	301	LGNIRAHNCISRAQWNNTLQIATTLREQFGNKTIAFNQSGGDPDEIVMHSFNCGEFF	360			
DB	333	LGNIRAHNCISRAQWNNTLQIATTLREQFGNKTIAFNQSGGDPDEIVMHSFNCGEFF	392			
QY	361	YCNSTOLFNSAMNVTSGTWSVTRKQDGTDIITLPCRKQIINRQVGVKAMYPKIG	420			
DB	393	YCNSTOLFNSAMNVTSGTWSVTRKQDGTDIITLPCRKQIINRQVGVKAMYPKIG	452			
QY	421	LIRCSSNITGLLLTRDGGGENOTTEIFRPGGGDMRDNWRSELYKYKVKIEPLGVAPTKA	480			

DB	453	LIRCSSNITGLLLTRDGGGENOTTEIFRPGGGDMRDNWRSELYKYKVKIEPLGVAPTKA	512			
QY	481	KRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOAROLLISGIVQOQNLLRAIK	540			
DB	513	KRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOAROLLISGIVQOQNLLRAIK	572			
QY	541	AQOHLQLTVMGTIKOLOARILAVERYLKDOQLLGFWGCSSGKLICTTAVPNASWSNKTLD	600			
DB	573	AQOHLQLTVMGTIKOLOARILAVERYLKDOQLLGFWGCSSGKLICTTAVPNASWSNKTLD	632			
QY	601	QIWNNTMWEWDREIDNYTHLIYTLIEESQNOQEKNOQELLQDLKXWASL	649			
DB	633	QIWNNTMWEWDREIDNYTHLIYTLIEESQNOQEKNOQELLQDLKXWASL	681			
RESULT 2						
Q7SVL3_9HIV1						
ID	Q7SVL3_9HIV1	PRELIMINARY;	PRT;	854 AA.		
AC	Q7SVL3_9HIV1	PRELIMINARY;	PRT;	854 AA.		
DT	01-OCT-2003	(T-EMBLrel. 25, Created)				
DT	01-OCT-2003	(T-EMBLrel. 25, Last sequence update)				
DT	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)				
DE	Envelope	glycoprotein.				
GN	Name=env;					
OS	Human immunodeficiency virus 1.					
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;					
OC	Lentivirus; Primate lentivirus group.					
OX	NCBI_TaxID=11676;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=22628496; PubMed=12743293;					
RX	DOI=10.1128/JVI.77.11.6359-6366.2003;					
RA	Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairaj A.S.,					
RA	Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;					
RT	"U.S. Human immunodeficiency virus type 1 epidemic: date of origin,					
RT	population history, and characterization of early strains.";					
RL	J. Virol. 77:6359-6366(2003).					
DR	EMBL; AY247222; AAP37150.1; -; Genomic_DNA.					
DR	HSSP; P04578; IDLB.					
DR	SMR; Q7SVL3; 2-154, 195-489, 538-624.					
DR	GO; GO:0016021; C:integral to membrane; IEA.					
DR	GO; GO:0019031; C:viral envelope; IEA.					
DR	GO; GO:0005198; F:structural molecule activity; IEA.					
DR	InterPro; IPR000328; Env.GP41.					
DR	InterPro; IPR000777; GP120.					
DR	Pfam; PF00516; GP120; 1.					
DR	Pfam; PF00517; GP41; 1.					
KW	AIDS; Envelope protein; Transmembrane.					
SQ	SEQUENCE 854 AA; 97048 MW; 36379231FF3AF12C CRC64;					
Query Match						
Best Local Similarity 84.3%; Score 2927; DB 2; Length 854;						
Matches 555; Conservative 33; Mismatches 45; Indels 16; Gaps 7;						
QY	3	LWTVYGVVYGVVKEATTTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE	62			
DB	33	LWTVYGVVYGVVKEATTTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE	92			
QY	63	NFMNKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSLIIVVW	122			
DB	93	NFMNKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCT--NLRNTNTTSS--WGT	146			
QY	123	ROKGEKMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNKTNTKYRLINCNTSVITQ	182			
DB	147	MESGEIKNCSPNITTSIRDKVQREYALFYKLDVWPINDD-NTT--TSYRLINCNTSVITQ	203			
QY	183	ACPVKSEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL	242			
DB	204	ACPVKSEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL	263			
QY	243	SLAEEVVIRSENFNTNNAKTIIVQLNVSVENCTRPNNHTRKRVTLGPGRVVYTTGEI	302			

Db 264 SLAEEVIRSDNFTDNTAKTIIVQLNESVEINCTPNNTRKSNIGPCRAFYATGEIIG 323
 QY 303 NIROAHCHNISRAQWNTLQOIAATTLREQFG-NKTIAPNOSGGDPEIIVMHSFNCGGEFFY 361
 Db 324 DIRQAHCHNLRAKWNMTLQIVTKLREQFGNKTIVFNOSGGDPEIIVMHSFNCGGEFFY 383
 QY 362 CNSTOLFNSANNVTSGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPKGL 421
 Db 384 CDSOLFNSWENDNN-----IRGSNSTQENITLPCRILQIINRWQVGVKAMYPKGL 438
 QY 422 IRCSNNTGLLITRDGG-GENOTTEIFRPGGDMRDNRSELYKYVVKIEPLGVAPTKA 480
 Db 439 IRCSNNTGLLITRDGGKDEGTTEIFRPGGDMRDNRSELYKYVVKIEPLGVAPTKA 498
 QY 481 KRRVQREKRAVGMFLGAMFLGAGSTMGATSMALTVQARQLLSGIVQOQNLLRAIK 540
 Db 499 KRRVQREKRAVGTIGAMFLGAGSTMGATSMALTVQARQLLSGIVQOQNLLRAIE 558
 QY 541 AQOHLQITVWGIKOQARILAVERYLKDQQLLGFWGSGKLICTTAVPWNASWSNKLD 600
 Db 559 AQOHLQITVWGIKQARVLAVERYLKDQQLLGFWGSGKLICTTAVPWNASWSNKSLD 618
 QY 601 QIWNMTWMEWDREIDNTNLIYTLIESQOENQOELLQDKWASL 649
 Db 619 KIWNMTWMEWEIDNTNLIYTLIESQOENQOELLQDKWASL 667

RESULT 3
 O40222_9HIV1 PRELIMINARY; PRT; 854 AA.
 ID O40222_9HIV1 PRELIMINARY; PRT; 854 AA.
 AC O40222;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Env polyprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AD8;
 RX MEDLINE=96432129; PubMed=8835195;
 RA Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
 RA Martin M.A., Peden K.W.;
 RT "Construction and characterization of a stable full-length macrophage-
 RT tropic HIV type 1 molecular clone that directs the production of high
 RT titers of progeny virions.";
 RL AIDS Res. Hum. Retroviruses 12:191-194(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AD8;
 RA Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
 RA Martin M.A., Peden K.W.C.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF004394; AAB64170.1; -; Genomic_DNA.
 DR HSSP; P04578; 1DLB.
 DR SMR; O40222; 143-489, 538-624.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Polyprotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97291 MW; 06C45B69103C6C12 CRC64;

Query Match 83.7%; Score 2908; DB 2; Length 854;
 Best Local Similarity 84.0%; Pred. No. 9,1e-22;
 Matches 548; Conservative 36; Mismatches 48; Indels 20; Gaps 7;

QY 2 NLWTVVYGVVWKEATITLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 61
 Db 32 NLWTVVYGVVWKEATITLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 91
 QY 62 FNMKNNVQOMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDL-NTNNTNTTETLSIIVW 120
 Db 92 FNMKNNVQOMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNVTNINNSSE----- 144
 QY 121 EQRQKGRNCSFNITTSIRDKVQREYALFKLDVEPIDDNKNTNTTKYRLINCNTSVI 180
 Db 145 --GMRGEIKNCSFNITTSIRDKVKQVALFYRLDVVPIDN-----DNTSYRLINCNTSTI 197
 QY 181 TQACPVSFEPIDPHYCTPTGFPALLKCKNDKFPNGTCTNVTSTVQCTHGIRPVVSTQLLL 240
 Db 198 TQACPVSFEPIDPHYCTPTGFPALLKCKNDKFPNGTCTNVTSTVQCTHGIRPVVSTQLLL 257
 QY 241 NGSIAEEVIRSNFTNNAKTIIVOLNVSVIEINCTRNHNTRKRVTLGPGRVVYTCEI 300
 Db 258 NGSIAEEVIRSNFTNNAKTIIVOLKESVEINCTRNHNTRKRVTLGPGRVVYTCEI 317
 QY 301 LGNIROAHCHNISRAQWNTLQOIAATTLREQFG-NKTIAPNOSGGDPEIIVMHSFNCGGEF 359
 Db 318 IGDIROAHCHNISRTKWNNTLQIATLKEQFGNKTIVFNOSGGDPEIIVMHSFNCGGEF 377
 QY 360 FYCNSOLFNSANNVTSGTWSVTRKQKDTG-DIITLPCRILQIINRWQVGVKAMYPKGL 418
 Db 378 FYCNSOLFNSWTF--NGTWNLTQSGNTEGNTITLPCRILQIINRWQVGVKAMYPKGL 435
 QY 419 KGLRCSNITGLLITRDGG-GENOTTEIFRPGGDMRDNRSELYKYVVKIEPLGVAP 477
 Db 436 RGQIRCSNITGLLITRDGGNNHNDTETFRPGGDMRDNRSELYKYVVKIEPLGVAP 495
 QY 478 TKAKRRVVQREKRAVGMFLGAMFLGAGSTMGATSMALTVQARQLLSGIVQOQNLLR 537
 Db 496 TKAKRRVVQREKRAVGTIGAMFLGAGSTMGATSMALTVQARQLLSGIVQOQNLLR 555
 QY 538 AIKAQOHLQITVWGIKOQARILAVERYLKDQQLLGFWGSGKLICTTAVPWNASWSNK 597
 Db 556 AIEAQOHLQITVWGIKQARVLAVERYLKDQQLLGFWGSGKLICTTAVPWNASWSNK 615
 QY 598 TLDQIWNMTWMEWDREIDNTNLIYTLIESQOENQOELLQDKWASL 649
 Db 616 TLDIWNMTWMEWEIDNTNLIYTLIESQOENQOELLQDKWASL 667

RESULT 4
 Q6UYR2_9HIV1 PRELIMINARY; PRT; 853 AA.
 ID Q6UYR2_9HIV1 PRELIMINARY; PRT; 853 AA.
 AC Q6UYR2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
 RA Kuhnmann S.E., Pugach P., Kunstan K.J., Taylor J., Stanfield R.L.,
 RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
 RA Korber B.T., Wolinsky S.M., Moore J.P.;
 RT "Genetic and phenotypic analyses of human immunodeficiency virus type
 RT 1 escape from a small-molecule CCR5 inhibitor.";
 RL J. Virol. 78:2790-2807(2004).
 DR EMBL; AY357520; AAR00883.1; -; Genomic_DNA.
 DR HSSP; P04578; 1K33
 DR SMR; Q6UYR2; 196-493, 541-627.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.

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DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 853 AA; 96993 MW; 7392EE340C50C4AD CRC64;

Query Match      83.7%; Score 2906.5; DB 2; Length 853;
Best Local Similarity 83.7%; Pred. No. 1.2e-221; Indels 13; Gaps 7;
Matches 543; Conservative 46; Mismatches 47;

Qy 3 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSELSIIVW-E 121
Db 93 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTD-DVRNATSTNS-----SWGK 146
Qy 122 QRGKGMKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVIT 181
Db 147 PMEKEIKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVIT 203
Qy 182 QACPKVSEPIPIHYCTPTGFALLKCNCKFKNGTGPCTNVSTVQCTHGIRPVVSTQLLN 241
Db 204 QACPKVSEPIPIHYCAPAGFALLKCNCKFKNGTGPCTNVSTVQCTHGIRPVVSTQLLN 263
Qy 242 GSLAEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEIL 301
Db 264 GSLAEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEIL 323
Qy 302 GNIQAHCNISRACNNTLQOIAATTLREOFG-NKTIAPNOSGGDPEIVMHSFNCGGEFF 360
Db 324 GDIQAHCNISRACNNTLQOIAATTLREOFG-NKTIAPNOSGGDPEIVMHSFNCGGEFF 383
Qy 361 YCNSTOLFNSAWNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYALPIK 420
Db 384 YCNSTKLFNSW-TWNSTWNNTKBSNDTBELITLPCRIKQIINRWQVGVKAMYALPIK 442
Qy 421 LIRCSSNITGLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTGA 480
Db 443 QIRCSSNITGLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTGA 502
Qy 481 KRRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRAIK 540
Db 503 KRRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRAIK 561
Qy 541 AQHLLQLTWGKIKQOARILAVERYLKDOQLLGFAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 600
Db 562 AQHLLQLTWGKIKQOARILAVERYLKDOQLLGFAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 621
Qy 601 QIWNNTMTWMDREIDNTHLYTLIESQKQKQOELLQDLKWSL 649
Db 622 EIWNNMTWMEKEIDNTHLYTLIESQKQKQOELLQDLKWSL 670

RESULT 5
Q7SVL7_9HIV1
ID Q7SVL7_9HIV1 PRELIMINARY; PRT; 860 AA.
AC Q7SVL7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22628496; PubMed=12743293;
RX
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RX DOI=10.1128/JVI.77.11.6359-6366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairaj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains.";
RL J. Virol. 77:6359-6366(2003).
DR EMBL; AY247218; AAP37146.1; -; Genomic_DNA.
DR HSP; P20871; ICE4.
DR SMR; Q7SVL7; 195-496, 541-630.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 860 AA; 97762 MW; A7E185F2BD421590 CRC64;

Query Match      83.6%; Score 2905; DB 2; Length 860;
Best Local Similarity 84.2%; Pred. No. 1.6e-221; Indels 14; Gaps 7;
Matches 548; Conservative 41; Mismatches 48;

Qy 3 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSELSIIVWVQ 122
Db 93 NMWKNVVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTSSS---GGK 146
Qy 123 RKGEMKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVITQ 182
Db 147 MEKEIKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVITQ 203
Qy 183 ACPKVSEPIPIHYCTPTGFALLKCNCKFKNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 204 ACPKVSEPIPIHYCTPAGFALLKCNCKFKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 263
Qy 243 SLAEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEILG 302
Db 264 SLAEEVIRSDNFMNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEILG 323
Qy 303 NTRQAHCNISRACNNTLQOIAATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFFC 362
Db 324 DIRQAHCNISRACNNTLQOIAATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFFC 383
Qy 363 NSTOLFNSAWN-VTSNGTW-SVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYALPIK 419
Db 384 DSTOLFNSAWN-TLSTWNTKBSNDTBELITLPCRIKQIINRWQVGVKAMYALPIK 443
Qy 420 GLIRCSSNITGLLTRDGG-GENQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 478
Db 444 QIRCSSNITGLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 503
Qy 479 KARRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 538
Db 504 KARRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 562
Qy 539 IKAQHLQLTWGKIKQOARILAVERYLKDOQLLGFAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 598
Db 563 IEAQHLQLTWGKIKQOARILAVERYLKDOQLLGFAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 622
Qy 599 LQIWNNTMTWMDREIDNTHLYTLIESQKQKQOELLQDLKWSL 649
Db 623 LDKIWNNTMTWMDREIDNTHLYTLIESQKQKQOELLQDLKWSL 673

RESULT 6
Q6UYPO_9HIV1
ID Q6UYPO_9HIV1 PRELIMINARY; PRT; 863 AA.
AC Q6UYPO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1490699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhlmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor."
RL J. Virol. 78:2790-2807(2004)
DR EMBL; AY357551; AAR00905.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYF0; 93-147, 209-507, 552-641.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER
SQ SEQUENCE 863 AA; 98144 MW; 02D82C72985648EC CRC64;

Query Match 83.5%; Score 2900.5; DB 2; Length 863;
Best Local Similarity 83.5%; Pred. No. 3.6e-221;
Matches 545; Conservative 45; Mismatches 50; Indels 13; Gaps 8;

QY 2 NLWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 61
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 40 NLWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 99
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 FNMKNVQWHEHDIISLWQSLKPCVKLPLCVTLNCTDLN--TNTNTTTELSIIIVW 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 100 FNMKNVQWHEHDIISLWQSLKPCVKLPLCVTLNCTDLN--TNTNTTTELSIIIVW 154
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 -EQKGMKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNTSV 179
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 155 GEPMEKEIKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNTSV 214
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 ITQACPKVSPFPIHYCTPTGFPALLKCKDKKFGTGPCTNVSTVQCTHGRPVVSTQLL 239
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 215 ITQACPKVSPFPIHYCAPAGFAILKCKDKKFGTGPCTNVSTVQCTHGRPVVSTQLL 274
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 LKNGSLAEBEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTGE 299
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 275 LKNGSLAEBEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTGE 334
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 ILGNIRQAHNCISRAQWNTLQIATTLREQFG-NKTIAPQSSGGDPEIVMHSFNCGGE 358
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 335 IIGDIRKAHCNISRAQWNTLKHIVKLGKQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 394
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 PFYCNSTQLFNSANWVTSNGTW--SVTRKQKDTGDIITLPCRKIQIINRWQVVKAMVAL 416
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 395 PFYCNSTQLFNSW--TWNNGTWTNRNTERSSTEEKITLPCRKIQIINRWQVVKAMVAL 453
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 417 PIKGLIRCSNITGLLLTRDGGGNOTTEIFRPGGDMRDNWSELVYKVKVLEPLGVA 476
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 454 PIKGLIRCSNITGLLLTRD--GGTNTNTETFRPGGDMRDNWSELVYKVKVLEPLGVA 512
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 477 PTKARRVVOREKRAVGLGAMFGLGAGSTMGATSMALTVOARQLLSGIVQQNNLL 536
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 513 PTEAKRRVVOREKRAVG-IGAVLGLGAGSTMGASVTLTVQARQLLSGIVQQNNLL 571
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 537 RAIKAQHLLQLTWGIKQLQARILAVERYLKDQQLGFWCCKGLICTTAVPWNASWN 596
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 572 RATEAQHLLQLTWGIKQLQARILAVERYLKDQQLGFWCCKGLICTTAVPWNASWN 631
QY 597 KTLDOIWNNTWMEWDREIDNYTHLYTLIEESQOQKQKQELQLDKWASL 649
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 632 KSMDEIWNNTWMEWKEIDNYTGLIYNLLEKSNQOQKQKQELQLDKWASL 684
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q7SVL5_9HIV1 PRELIMINARY; PRT; 852 AA.
AC Q7SVL5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22628496; PubMed=12743293;
RX DOI=10.1128/JVI.77.11.6359-6366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kallish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains.";
RL J. Virol. 77:6359-6366(2003)
DR EMBL; AY247220; AAP37148.1; -; Genomic_DNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7SVL5; 536-622.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 852 AA; 96680 MW; F8D811028035D998 CRC64;

Query Match 83.4%; Score 2899; DB 2; Length 852;
Best Local Similarity 83.9%; Pred. No. 4.7e-221;
Matches 546; Conservative 36; Mismatches 47; Indels 22; Gaps 6;

QY 3 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 33 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 NMWKNVQWHEHDIISLWQSLKPCVKLPLCVTLNCTDLNNTNTNTTTELSIIIVWEQ 122
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 93 NMWKNVQWHEHDIISLWQSLKPCVKLPLCVTLNCTDLN--GNTNTTSS----- 143
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 RG----KGMKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNTS 178
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 144 -GGMERGEIKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNTS 197
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 VITQACPKVSPFPIHYCTPTGFPALLKCKDKKFGTGPCTNVSTVQCTHGRPVVSTQL 238
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 198 VITQACPKVSPFPIHYCAPAGFAILKCKDKKFGTGPCTNVSTVQCTHGRPVVSTQL 257
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 LKNGSLAEBEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTG 298
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 258 LKNGSLAEBEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTG 317
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 EILGNIRQAHNCISRAQWNTLQIATTLREQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 358
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 DIVGDIRQAHNCISRAQWNTLQIATTLREQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 377
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 PFYCNSTQLFNSANWVTSNGTW--SVTRKQKDTGDIITLPCRKIQIINRWQVVKAMVAL 418
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 PFYCNSTQLFNSW--TWNDEGSNTTEGTTLPCRKIQIINRWQVVKAMVAL 435
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 419 KGLRCSNITGLLLTRDGGGENOTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
D 436 RGQIRCSNITGLLLTRDGGSENDTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 495
QY 479 KAKRVVQREKRAVGMGLAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 538
D 496 KAKRVVQREKRAVG-IGAVFLGFLGAGSTMGAASTLTVOARQLLSGIVQQNNLLRA 554
QY 539 IKAQHLLQLTVMGKIQOLQARILAVERYLKDOQLLGFNGCGSKLICCTAVPNAWSNKT 598
D 555 IEAQHLLQLTVMGKIQOLQARVLAVERYLKDOQLLGFNGCGSKLICCTAVPNAWSNKS 614
QY 599 LDOIWNNTWMEWDREIDNTHLYTLIESQNOQKNOQELLQDKWASL 649
D 615 LDNIWNNTWMEWDREINNTSLYTLIESQNOQKNEQELLELDKWASL 665

RESULT 8
Q6UYM7_9HIV1
ID Q6UYM7_9HIV1 PRELIMINARY; PRT; 869 AA.
AC Q6UYM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1126/JVI.78.6.2790-2807.2004;
RA Kuhnman S.E., Pugach P., Kunsman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizky J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357566; AAR00918.1; -; Genomic_DNA.
DR SBL; Q6UYM7; 90-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 869 AA; 99123 MW; FE2BE1E50EF1CC9A CRC64;

Query Match 83.4%; Score 2896.5; DB 2; Length 869;
Best Local Similarity 82.5%; Pred. No. 5.3e-221;
Matches 543; Conservative 48; Mismatches 50; Indels 17; Gaps 8;

QY 2 NLWVTYVYGVVWKKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 61
D 40 NLWVTYVYGVVWKKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 99
QY 62 FNNWKNMVQEMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL---NTNNTNTTSLIIV 118
D 100 FNNWKNMVQEMHEDIISLWDQSLKPCVKLTPLCVTLNCTDYVKNATNTTN----- 154
QY 119 VW-EQKRGKMRNCSEFNITTSIRDKVQREYALFYKLDVEPID--NKNTTN---TKYRL 172
D 155 SWGEPMEKGEIKNCSEFNITTSIRDKVQREYALFYKLDVEPIDNDSNNNSNNNYNYRL 214
QY 173 INCNTSVITQACPKVSEFPIPIHYCTPTGPAKLCNDKFKNGTGPCTNSTVQCTHGIRP 232
D 215 INCNTSVITQACPKVSEFPIPIHYCAPAGPAKLCNDKFKNGTGPCTNSTVQCTHGIRP 274

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QY 233 VVSTQLLNGSLAEVEEVIRESNFTNNAKTIIVQLNVSVSEINCTRPNNHTRKRVTLGPGR 292
D 275 VVSTQLLNGSLAEVEEVIRESNFTNNAKTIIVQLNVSVSEINCTRPNNHTRKRVTLGPGR 334
QY 293 VVYTTGEILGNITROAHNCNISRAQNNNTLQOQIATTLREQFGNKTIAFNQSSGGDPEIVMHS 352
D 335 VVYTTGEIVGDIRKAHCNISRTQNNNTLKHIVEKLGKQFGNNKTIFNHSSGGDPEIVMHS 394
QY 353 FNCGGFFFCYNSTQLFNSANWVTSNGTSWTRKQKDTGDIITLPCRIKQIINWQVVGKA 412
D 395 FNCGGFFFCYNSTKLFNSTW--TRNNDTW--TERSNSTEHEITLPCRIKQIINWQVVGKA 452
QY 413 MYALPIKGLIRCSNITGLLLTRDGG-GENOTTEIFRPGGDMRDNRSELYKYKVKIE 471
D 453 VIAPPTRGKIRCSNITGLLLTRDGGNNDTRGTEIFRPGGDMRDNRSELYKYKVKIE 512
QY 472 PLGVAPTAKRRVQREKRAVGMGLAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQ 531
D 513 PLGIAPTEAKRRVQREKRAVGMGLAMFLGFLGAGSTMGAASTLTVOARQLLSGIVQQ 572
QY 532 QNNLIRAIKAOQHLLQLTVMGKIQOLQARILAVERYLKDOQLLGFNGCGSKLICCTAVPWN 591
D 573 QNNLIRAIKAOQHLLQLTVMGKIQOLQARILAVERYLKDOQLLGFNGCGSKLICCTAVPWN 632
QY 592 ASWSNKTLDQIWNNTWMEWDREIDNTHLYTLIESQNOQKNOQELLQDKWASL 649
D 633 ASWSNRSIDEIWNNTWMEWEKEIDNTHLYTLIESQNOQKNEQELLELDKWANL 690

RESULT 9
Q03811_9HIV1
ID Q03811_9HIV1 PRELIMINARY; PRT; 853 AA.
AC Q03811;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface envelope glycoprotein.
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91195299; PubMed=2014229;
RA Westervelt P., Gendelman H.E., Ratner L.;
RT "Identification of a determinant within the human immunodeficiency
RT virus 1 surface envelope glycoprotein critical for productive
RT infection of primary monocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3097-3101(1991).
DR EMBL; M50472; AAA45065.1; -; Genomic_RNA.
DR HSSP; P20871; 1CE3.
DR SMR; Q03811; 143-488, 537-623.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 853 AA; 96998 MW; AD2AF21E2B06AD78 CRC64;

Query Match 83.4%; Score 2896.5; DB 2; Length 853;
Best Local Similarity 83.6%; Pred. No. 7.4e-221;
Matches 544; Conservative 40; Mismatches 48; Indels 19; Gaps 6;

QY 2 NLWVTYVYGVVWKKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 61
D 32 NLWVTYVYGVVWKKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 91
QY 62 FNNWKNMVQEMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL-NTNNTNTTSLIIVW 120
D 92 FNNWKNMVQEMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLRNVTNNNSSE----- 144

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DR HSP; P20871; 1CE4.
DR SMR; Q7SVL4; 195-486, 534-620.
DR GO; 0016021; C: integral to membrane; IEA.
DR GO; 0019031; C: viral envelope; IEA.
DR GO; 00005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 850 AA; 96583 MW; 62ED5F6AB033D20B CRC64;

Query Match 83.3%; Score 2895; DB 2; Length 850;
Best Local Similarity 84.9%; Pred. No. 9.7e-221;
Matches 552; Conservative 33; Mismatches 43; Indels 22; Gaps 8;

Qy 3 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db |||||
Qy 33 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 92
Db |||||
Qy 63 NMWKNNVVEQMHEDIISLWDSQSKPCVKLPLCVLTNCTDLNNTNTTNTTSLSIIVWEQ 122
Db |||||
Qy 93 NMWKNNVVEQMHEDIISLWDSQSKPCVKLPLCVLTNCTDLNNTNTTSSS-----GGT 146
Db |||||
Qy 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 182
Db :|||:|
Qy 147 MERGEIKNCSFNITTSIRDKVQREYALFYKLDVPI-DNDNTT--TSYRLISCNTSVITQ 203
Db |||||
Qy 183 ACPKVSEPIPIHYCTPTGFPALLKCNKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 242
Db |||||
Qy 204 ACPKVSEPIPIHYCTPTGFPALLKCNKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 263
Db |||||
Qy 243 SLAEVVIRSENFTNNAKTIIVQNVSEINCTRPNNHTRKRVTLGPRVWVTGTEILG 302
Db |||||
Qy 264 SLAEVVIRSDNFDNAKTIIVQNVSEINCTRPNNHTRKRVTLGPRVWVTGTEILG 323
Db |||||
Qy 303 NIQAHCNISRAQWNTLQOIATTLREQFGKTIATFNQSSGGDPEIVMHSFNCGGFFYC 362
Db :|||:|
Qy 324 DIRQAHCNLSRAQWNTLQOIATTLREQFGKTIATFNQSSGGDPEIVMHSFNCGGFFYC 383
Db |||||
Qy 363 NSTOLFNSANVT--SNGTWSVTRKQKDTGDI-ITLPCRKQIINRWQVVGKAMYPALPK 419
Db :|||:|
Qy 384 DSTOLFNSANVT--SNGTWSVTRKQKDTGDI-ITLPCRKQIINRWQVVGKAMYPALPK 434
Db |||||
Qy 420 GLRCSNITGLLITRDGGNGEITLFRPGGDMRDNRSELYKYKVKIEPLGVAPTK 479
Db |||||
Qy 435 GQIRCSNITGLLITRDGGNGEITLFRPGGDMRDNRSELYKYKVKIEPLGVAPTK 494
Db |||||
Qy 480 AKRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAI 539
Db |||||
Qy 495 AKRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAI 553
Db |||||
Qy 540 KAQHLQLTQVGIKQIARILAVERYLKDQQLLGGFWGCGSKLICCTTAVPNWASWNTKL 599
Db :|||:|
Qy 554 EAQHLQLTQVGIKQIARILAVERYLKDQQLLGGFWGCGSKLICCTTAVPNWASWNTKL 613
Db |||||
Qy 600 DOIWNNTWMEDEIDNYTHLYTLIEESQNOQKQOELLQIDKWASL 649
Db |||||
Qy 614 DKIWNNWMEDEIDNYTHLYTLIEESQNOQKQOELLQIDKWASL 663
Db |||||

RESULT 12
Q7SVL4_9HIV1
ID Q7SVL4_9HIV1 PRELIMINARY; PRT; 861 AA.
AC Q7SVL4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.

OX NCB1_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22533916; PubMed=12646921; DOI=10.1038/nature01470;
RA Wei X., Decker J.M., Wang S., Hui H., Kappes J.C., Wu X.,
RA Salazar-Gonzalez J.F., Salazar M.G., Kilby J.M., Saag M.S.,
RA Komarova N.L., Nowak M.A., Hahn B.H., Kwong P.D., Shaw G.M.;
RT "Antibody neutralization and escape by HIV-1.";
RL Nature 422:307-312(2003).
DR ENBL; AY223724; AAP57324.1; -; Genomic_RNA.
DR HSP; P04578; IDLB.
DR SMR; Q7SVL4; 545-631.
DR GO; 0016021; C: integral to membrane; IEA.
DR GO; 0019031; C: viral envelope; IEA.
DR GO; 00005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 861 AA; 98313 MW; 4E8A3F4278A9E302 CRC64;

Query Match 83.3%; Score 2893.5; DB 2; Length 861;
Best Local Similarity 83.1%; Pred. No. 1.3e-220;
Matches 544; Conservative 42; Mismatches 50; Indels 19; Gaps 7;

Qy 2 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 61
Db |||||
Qy 32 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 91
Db |||||
Qy 62 FMWKNNVVEQMHEDIISLWDSQSKPCVKLPLCVLTNCTDLNNTNTTNTTSLSIIVWE 121
Db |||||
Qy 92 FMWKNNVVEQMHEDIISLWDSQSKPCVKLPLCVLTNCTDLNNTNTTNTTSLSIIVWE 144
Db |||||
Qy 122 QRGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVIT 181
Db :|||:|
Qy 145 REMRGEIKNCSFNITTSIRDKVQREYALFYKLDVPI-DNDNTTNTTNTTSLSIIVWE 201
Db |||||
Qy 182 QACPKVSEPIPIHYCTPTGFPALLKCNKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 241
Db |||||
Qy 202 QACPKVSEPIPIHYCTPTGFPALLKCNKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 261
Db |||||
Qy 242 GSLAEVVIRSENFTNNAKTIIVQNVSEINCTRPNNHTRKRVTLGPRVWVTGTEIL 301
Db |||||
Qy 262 GSLAEVVIRSENFTNNAKTIIVQNVSEINCTRPNNHTRKRVTLGPRVWVTGTEIL 321
Db |||||
Qy 302 GNIRQAHCNISRAQWNTLQOIATTLREQFG-NKTIATFNQSSGGDPEIVMHSFNCGGFF 360
Db :|||:|
Qy 322 GDIRQAHCNISRAQWNTLQOIATTLREQFG-NKTIATFNQSSGGDPEIVMHSFNCGGFF 381
Db |||||
Qy 361 YCNSTOLFNSANVT--SNGTWSVTRKQKDTGDI-ITLPCRKQIINRWQVVGKAMYA 415
Db |||||
Qy 382 YCNSTOLFNSANVT--SNGTWSVTRKQKDTGDI-ITLPCRKQIINRWQVVGKAMYA 439
Db |||||
Qy 416 LPTKGLIRCSNITGLLITRDGGNGEITLFRPGGDMRDNRSELYKYKVKIEPLG 474
Db |||||
Qy 440 PPIRQIRCSNITGLLITRDGGNGEITLFRPGGDMRDNRSELYKYKVKIEPLG 499
Db |||||
Qy 475 VAPTAKRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNN 534
Db |||||
Qy 500 VAPTAKRRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNN 559
Db |||||
Qy 535 LLRAIKAOHLQLTQVGIKQIARILAVERYLKDQQLLGGFWGCGSKLICCTTAVPNWASW 594
Db |||||
Qy 560 LLRAIKAOHLQLTQVGIKQIARILAVERYLKDQQLLGGFWGCGSKLICCTTAVPNWASW 619
Db |||||
Qy 595 SNKTLDOIWNNTWMEDEIDNYTHLYTLIEESQNOQKQOELLQIDKWASL 649
Db |||||
Qy 620 SNRSLDDIWHNNWMEDEIDNYTHLYTLIEESQNOQKQOELLQIDKWASL 674
Db |||||

RESULT 13
Q6UYPL_9HIV1

Q6UYPI_9HIV1 PRELIMINARY; PRT; 867 AA.
Q6UYPI: 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment)
Name-env;
GN Human immunodeficiency virus 1.
OS Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:1490899; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhn M.S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strick J., Riley J., Baroud B.M., Wilson I.A.,
RA Koerber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357550; AAR00904.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; G6UYPI_93-147, 209-511, 559-645.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 867 AA; 98541 MW; F14F0B3372EC7C6D CRC64;

Query Match 83.3%; Score 2892.5; DB 2; Length 867;
Best Local Similarity 83.1%; Pred. No. 1.6e-220;
Matches 545; Conservative 44; Mismatches 52; Indels 15; Gaps 8;

Qy 2 NLWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTEN 61
Db 40 NLWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTEN 99

Qy 62 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTSLIIVV 120
Db 100 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDKNTNNATNTS----SW 154

Qy 121 -EQRGKGMRCNSFNITTSIRDKVOREYALFYKLDVEPIDDKNTTNTKRLNCNTSV 179
Db 155 GEPMEKGEIKNCNSFNITTSIRDKVOREYALFYKLDVVPIDNDNNNTNNTYRLISCN 214

Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 239
Db 215 ITQACPKVSEPIPIHYCAPAGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 274

Qy 240 LNSLAEEVVRIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 275 LNSLAEEVVRIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 334

Qy 300 ILGNIRQAHCHISRAQWNTLQOATTLREBFG-NKTIAFNQSSGGDDEIVMHSFNCGGE 358
Db 335 IIGDIRKAHCNISRAQWNTLKHIVEKLQFGNKKTVFVHSSGGDDEIVMHSFNCGGE 394

Qy 359 PFYCNSTOLFNSANVTSNGTW--SVTRKQKDTGDIITLPCRIKOINRWQVGVKMYAL 416
Db 395 PFYCNSTOLFNSANVTSNGTW--SVTRKQKDTGDIITLPCRIKOINRWQVGVKMYAL 453

Qy 417 PIKGLIRCSSNITGLITRDGGGNOT---TEIFRPGGDMRDNRSELYKYKVVKIEPL 473
Db 454 PIKGLIRCSSNITGLITRDGGGNOT---TEIFRPGGDMRDNRSELYKYKVVKIEPL 513

Qy 474 GVAPTKAKRVVQREKRAVGLGAMFLGFLGAAGSTMGATSMALTVQARLLSGIVQOQN 533
Db 514 GVAPTKAKRVVQREKRAVGLGAMFLGFLGAAGSTMGATSMALTVQARLLSGIVQOQN 572

Qy 534 NLLRAIKAQOHLLOLTWVGIKQIQARILAVERYLKQOLLGFWGCSGKLICTTAVPNNAS 593
Db 573 NLLRAIKAQOHLLOLTWVGIKQIQARILAVERYLKQOLLGFWGCSGKLICTTAVPNNAS 632

Qy 594 WSNKTLDOINWNTMDEIDNYTHLYTLIESONQOQEKNOELLQDLQKWSL 649
Db 633 WSNKSMDEINWNTMDEIDNYTHLYTLIESONQOQEKNOELLQDLQKWSL 688

RESULT 14
Q52S58_9HIV1 PRELIMINARY; PRT; 851 AA.
AC Q52S58;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Envelope glycoprotein.
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H434;
RA Geels M.J., Jansen C., Baan E., De Cuyper I.M., van Schijndel G.J.M.,
RA Pollakis G., Schuitemaker H., Bakker M., Goudemits J., van Baarle D.,
RA Paxton W.A., Miedema F.;
RT "Differential loss of human immunodeficiency virus type 1 (HIV-1) -
RT specific T-helper responses in two HIV-1 infected individuals
RT following CTL escape.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY970947; AAX86729.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 851 AA; 96407 MW; A447B60789932CF7 CRC64;

Query Match 83.2%; Score 2890.5; DB 2; Length 851;
Best Local Similarity 83.5%; Pred. No. 2.2e-220;
Matches 550; Conservative 35; Mismatches 35; Indels 39; Gaps 9;

Qy 3 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTENF 62
Db 33 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTENF 92

Qy 63 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTSLIIVV 119
Db 93 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTSLIIVV 148

Qy 120 WEORGKGMRCNSFNITTSIRDKVOREYALFYKLDVEPIDDKNTTNTKRLNCNTSV 179
Db 149 WGE-----EMTNCNSFNITTSIRDKVOREYALFYKLDVVPID--KNT---TKRLNCNTSV 199

Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 239
Db 200 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 259

Qy 240 LNSLAEEVVRIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 260 LNSLAEEVVRIRSENFNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 319

Qy 300 ILGNIRQAHCHISRAQWNTLQOATTLREBFGNKKTVFVHSSGGDDEIVMHSFNCGGE 359
Db 320 IIGDIRKAHCNISRAQWNTLKHIVEKLQFGNKKTVFVHSSGGDDEIVMHSFNCGGE 379

Qy 360 FYCNSTOLFNSANVTSNGTW--SVTRKQKDTGDIITLPCRIKOINRWQVGVK 411
Db 380 FYCNSTOLFNSANVTSNGTW--SVTRKQKDTGDIITLPCRIKOINRWQVGVK 425

Qy 412 AMYALPIKGLIRCSSNITGLITRDGGG-NOTTEIFRPGGDMRDNRSELYKYKVVKI 470
Db 426 AMYALPIKGLIRCSSNITGLITRDGGG-NOTTEIFRPGGDMRDNRSELYKYKVVKI 485


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Qy 471 EPLGVAPTKARRVVOREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQ 530
Db 486 EPLGVAPTKARRVVOREKRAVGTIGAMFLGFLGAAGSTMGAAVALTVQARQLLSGIVQ 545
Qy 531 QONNLLRAIKAAQHLLQITVWGIKQARILAVERYLKDQQLGFWGCSGKLICTTAVPW 590
Db 546 QONNLLRAIEAQHLLQITVWGIKQARILAVERYLKDQQLGFWGCSGKLICTTAVPW 605
Qy 591 NASMSNTLDQIWNMTWMEWDREIDNYTHLYTLIEESQOQEKNOQELLQDKWASL 649
Db 606 NASMSNLSKNIWNTWMEWEREIENTSLIYTLIEEPQOQEKNEQELLEDDKWASL 664

RESULT 15
Q6UVN6_9HIV1 PRELIMINARY; PRT; 865 AA.
AC Q6UVN6_9HIV1 PRELIMINARY; PRT; 865 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhlmann S.E., Pugach P., Kunatman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357555; AAR00909.1; -; Genomic_DNA.
DR SMR; Q6UVN6; 93-147, 557-643.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER
SQ SEQUENCE 865 AA; 98421 MW; 9CB631053888C207 CRC64;
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Query Match 83.2%; Score 2889.5; DB 2; Length 865;
Best Local Similarity 83.0%; Pred. No. 2.7e-220;
Matches 543; Conservative 46; Mismatches 52; Indels 13; Gaps 8;
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Qy 2 NLAVTVYGVVPVKEATTTLLFCASDAKAYDTEAHNVWATHACVPTNPNOEVVLENVTEN 61
Db 40 NLAVTVYGVVPVKEATTTLLFCASDAKAYDTEAHNVWATHACVPTNPNOEVVLENVTEN 99
Qy 62 FNMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLN-TNNTNTTSLIIVW 120
Db 100 FNMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDKNTNNAATSTNSR-----W 154
Qy 121 -EQRGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCTSV 179
Db 155 GEPMEKEIKNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCTSV 214
Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNDFKNGTGPCTNVSTVQCTHGIRPWSQTLL 239
Db 215 ITQACPKVSEPIPIHYCAPAGFALLKCNKFKNGTGPCTNVSTVQCTHGIRPWSQTLL 274
Qy 240 LNSGLAEVEVIRSENFNTNAKIIIVQLNVSVSEINCTRPNNHTRKRVLPGRVWYTTGE 299
Db 275 LNSGLAEKEVIRSENFNTNAKIMVQLNVSVSEINCTRPNNHTRKRVLPGRVWYTTGE 334
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Qy 300 ILGNIRQAHCNISRAQNNNTLQOIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGE 358
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Qy 359 PFCNSTQLPNSAWNTVSGTWSV--TRKQKDTGDIITLPCRKIQIINRWQVVGKAMAYAL 416
Db 395 PFCNSTKLFPNSTW-TRKNGTWTNPDTERSNSTEHIITLPCRKIQIINRWQVVGKAMAYAP 453
Qy 417 PIKGLIRCSSNITGLLLTRDGGGENOT-TEIFRPGGDMRDNRSELYKYKVKVIBPLGV 475
Db 454 PIRGKIRCSSNITGLLLTRDGGNNDTSGTEIFRPGGDMRDNRSELYKYKVKVIBPLGI 513
Qy 476 APTKAKRRVVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOONNL 535
Db 514 APTKAKRRVVQREKRAVG-IGAMFLGFLGAGSTMGAAVTLTVQARLLLSGIVQOONNL 572
Qy 536 LRAIKAQHLLQLTVWGIKQARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWS 595
Db 573 LRAIEAHQHLLQLTVWGIKQARVLAVERYLRDQQLGFWGCSGKLICTTAVPWNASWS 632
Qy 596 NKTLDOIWNMTWMEWDREIDNYTHLYTLIEESQOQEKNOQELLQDKWASL 649
Db 633 NKSMDEIWNMTWMEWEKEIDNYTGLIYNLLEKSQOQEKNEQELLQDKWANL 686
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Job time : 299.698 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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(without alignments)
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Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2883.5	83.0	847	2	US-09-476-242-2
2	2852	82.1	850	1	US-08-448-603A-28
3	2852	82.1	850	2	US-09-134-075-28
4	2852	82.1	850	2	US-09-492-739-28
5	2852	82.1	850	2	US-09-966-931A-28
6	2834	81.6	855	1	US-08-022-835-6
7	2834	81.6	855	1	US-08-388-809-6
8	2834	81.6	855	1	US-08-647-714-6
9	2827.5	81.4	843	2	US-09-602-864-13
10	2818	81.1	855	2	US-07-956-483-14
11	2814.5	81.0	826	1	US-08-375-510-2
12	2814.5	81.0	826	1	US-08-487-657-2
13	2814.5	81.0	854	2	US-09-309-572-23
14	2814.5	81.0	854	2	US-09-718-096-23
15	2814	81.0	880	1	US-08-788-815-7
16	2814	81.0	880	2	US-09-157-963-7
17	2814	81.0	880	2	US-09-568-105-7
18	2809.5	80.9	856	1	US-07-916-098A-2
19	2809.5	80.9	856	1	US-09-476-242-1
20	2809.5	80.9	857	1	US-08-448-603A-30
21	2809.5	80.9	857	2	US-09-134-075-30
22	2809.5	80.9	857	2	US-09-492-739-30
23	2809.5	80.9	857	2	US-09-966-931A-30
24	2807.5	80.8	855	2	US-07-956-483-15
25	2806.5	80.8	856	2	US-09-124-900-9
26	2806.5	80.8	863	2	US-08-463-210-11
27	2806.5	80.8	863	2	US-08-463-028-11

28	2806.5	80.8	863	2	US-08-463-209-11	Sequence 11, Appl
29	2795.5	80.5	856	2	US-09-337-387-11	Sequence 11, Appl
30	2795.5	80.5	856	2	US-10-196-515-11	Sequence 11, Appl
31	2795	80.5	861	1	US-08-127-499A-14	Sequence 14, Appl
32	2795	80.5	861	1	US-08-482-847-14	Sequence 14, Appl
33	2795	80.5	861	2	US-07-956-483-10	Sequence 10, Appl
34	2795	80.5	861	2	US-08-472-240A-1	Sequence 7, Appl
35	2795	80.5	861	2	US-08-472-240A-7	Sequence 1, Appl
36	2795	80.5	861	2	US-08-817-441-103	Sequence 103, App
37	2787	80.2	861	2	US-07-956-483-16	Sequence 16, Appl
38	2786.5	80.2	865	2	US-07-956-483-13	Sequence 13, Appl
39	2781.5	80.1	887	2	US-08-472-240A-5	Sequence 5, Appl
40	2781	80.1	665	1	US-08-448-603A-32	Sequence 32, Appl
41	2781	80.1	665	2	US-09-134-075-32	Sequence 32, Appl
42	2781	80.1	665	2	US-09-492-739-32	Sequence 32, Appl
43	2781	80.1	665	2	US-09-966-931A-32	Sequence 32, Appl
44	2780	80.0	657	2	US-09-256-194-2	Sequence 2, Appl
45	2772	79.8	635	2	US-09-536-977-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-09-476-242-2
; Sequence 2, Application US/09476242
; Patent No. 6689879
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTOG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605.002
; CURRENT APPLICATION NUMBER: US/09/476.242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-476-242-2

Query Match	83.0%	Score 2883.5;	DB 2;	Length 847;
Best Local Similarity	83.3%	Pred. No. 1.5e-229;		
Matches	544;	Conservative	40;	Mismatches 38;
				Indels 31;
				Gaps 7;
Qy	3	LWTVYGVVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF	62	
Db	33	LWTVYGVVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF	92	
Qy	63	NMWKNNVQMHEDIISLDOSLKPCKVLTPLCVTLNCTDLNNTNTTNTTSLIIVVWQ	122	
Db	93	NMWKNNVQMHEDIISLDOSLKPCKVLTPLCVTLNCTDLNNTNTTNTTSLIIVVWQ	146	
Qy	123	RGKEMRNCSPNITTSIRDKVQREYALFYKLDVPEIDNNKNTNTNTKYRLNCTSVITQ	182	
Db	147	MDRGEIKNCSPKVTTSIRNKQKEYALFYKLDVVPIDN-----DNTSYKLNCNTSVITQ	201	
Qy	183	ACPKVSEPIPIHYCTPTGPFALLKCNKDKNGTGFCTNVTSTVQCTHGRPVVSTQLLNG	242	
Db	202	ACPKVSEPIPIHYCAPAGFAILLKCNKDKNGTGFCTNVTSTVQCTHGRPVVSTQLLNG	261	
Qy	243	SLAEEVVRSENTNNAKTIIVOLNVSVENCTFRPNNTHTKRVTLGPRVWYTTGILG	302	
Db	262	SLAEEVVRSENTNNAKTIIVOLNVSVENCTFRPNNTHTKRVTLGPRVWYTTGILG	321	
Qy	303	NIRQHCNISRAQWNTLQIATTLRFQGNKTIATFNQSSGGDPEIVHNSFCGGEFFYC	362	
Db	322	DIRQHCNISRAQWNTLQIATTLRFQGNKTIATFNQSSGGDPEIVHNSFCGGEFFYC	381	
Qy	363	NSTOLFNSAMVNT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWVGVKAMVALP	417	

Db 382 NSTOLFNSNTWNTGPNNTNGT-----ITLPCRIKQIINRWQVGVKAMYAPP 428
Qy 418 IKGLIRCSNITGLLLTRDGGGE-NOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVA 476
Db 429 IRGQIRCSNITGLLLTRDGGKEISNTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVA 488
Qy 477 PTKAKRRVVQREKRAVGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOONLL 536
Db 489 PTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSILTITVOARQLLSGIVQOONLL 547
Qy 537 RAIKAAQHLLQITVWGIKQOARILAVERYLKDOQLLGFWCGSKLICITTAVPWNASWSN 596
Db 548 RAIKAAQHLLQITVWGIKQOARILAVERYLKDOQLLGFWCGSKLICITTAVPWNASWSN 607
Qy 597 KTLDOQWNNMTWMEWDREIDNTHLYTLIESQOQEKNOQELLDKWSL 649
Db 608 KSLDOQWNNMTWMEWDREIDNTHLYTLIESQOQEKNOQELLDKWSL 660

RESULT 2
US-08-448-603A-28
; Sequence 28, Application US/08448603A
; Patent No. 5864027
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,603A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/072,833
; FILING DATE: 07-JUN-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-448-603A-28

Query Match 82.1%; Score 2852; DB 1; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

Qy 3 LWTVVYGVVWKEATITLFCASDAKAYDTFAHNVWATHACVTPNPNQVWLENVTENF 62
Db 33 LWTVVYGVVWKEATITLFCASDAKAYDTFAHNVWATHACVTPNPNQVWLENVTENF 92
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNAINTTSSS-----WGK 146

Db 93 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNAINTTSSS-----WGK 146
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Db 147 MERGEIKNCSFNVTTSIRDKMNEYALFYKLDVVVIDN-----DNTSYRLISCNTSVITQ 201
Qy 183 ACPRVSPPEPIPIHYCTPTGFALLKCNDDKFGNGTGPCTNVTVOCTHGRPVPVSTQLLNG 242
Db 202 ACPRVSPPEPIPIHYCAPAGFALLKCRDKKFGNGTGPCTNVTVOCTHGRPVPVSTQLLNG 261
Qy 243 SLAEEVVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
Db 262 SLAEEVVIRSANFSDNAKTIIVQLNESVEINCTRPNNHTRRSIHIGGRAFYATGIIIG 321
Qy 303 NIRQAHNCISRAOWNNTLOQIATTLREOFGNKTIAFNQSSGGDEPIVHHSFNCGGEFFYC 362
Db 322 DIRQAHNCNLSTKWNNTLKQIVTKLRHF-NKTIIVFNHSSGGDEPIVHHSFNCGGEFFYC 380
Qy 363 NSTOLFNSAMNVTSGTWSVTRKQKOTGDIITLPCRIKQIINRWQVGVKAMYALPIKGLI 422
Db 381 NTPPLFNSWTNYYT--TWNTEGSDNDCRNITLQCRIKQIINMWQEVGKAMYPPIRGQI 438
Qy 423 RCSSNITGLLLTRDGGGENOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPTAKR 482
Db 439 RCSSNITGLLLTRD-GGNNSETEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPTAKR 497
Qy 483 RVVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOONLLRAIKAO 542
Db 498 RVVQREKRAVG-IGAVFLGFLGAAGSTMGAASVTLTVQARLLLSGIVQOONLLRAIEAE 556
Qy 543 QHLLQLTVWGIKQOARILAVERYLKDOQLLGFWCGSKLICITTAVPWNASWSNKTLDQI 602
Db 557 QHLLQLTVWGIKQOARILAVERYLKDOQLLGFWCGSKLICITTAVPWNASWSNKSUDKI 616
Qy 603 WNNMTWMEWDREIDNTHLYTLIESQOQEKNOQELLDKWSL 649
Db 617 WNNMTWMEWDREIDNTHLYTLIESQOQEKNOQELLDKWSL 663

RESULT 3
US-09-134-075-28
; Sequence 28, Application US/09134075
; Patent No. 6042836
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,603
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000


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Db 557 QHLLQLTVWGIKQOLQARVLAVERYLKDQQLLGIWCGSGKLICTTAVPWNASWNSKSLDKI 616
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RESULT 5
US-09-966-931A-28
; Sequence 28, Application US/09966931A
; Patent No. 6806055
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931A
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-966-931A-28

Query Match 82.1%; Score 2852; DB 2; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

Qy 3 LWTVVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVTPNPQEVLENVTENF 62
Db 33 LWTVVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVTPNPQEVLENVTENF 92
Qy 63 NMWKNNVQOMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNTNTNTTSLIIVWEQ 122
Db 93 NMWKNNVQOMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNATNTSSS----WGK 146
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNSTVITQ 182
Db 147 MERGEIKNCSENVVTSIRDKMKEYALFYKLDVVPIDN-----DNISYRLISCNSTVITQ 201
Qy 183 ACPKVSPEPIPIHYCTPTGTFALLKCNCKNGKNGTGTCTNNVSTVQCTGTHGIRPVWSTQLLNG 242
Db 202 ACPKVSPEPIPIHYCAPAGFAILKCRDKKFGTGTCTNNVSTVQCTGTHGIRPVWSTQLLNG 261
Qy 243 SLAEEVWVIRSENFNTNNAKTIIVQLNVSVINCTRPNNHTKRVTLLGPGRVWVYTTGILG 302

Db 262 SLAEEVWVIRSENFSDNAKTIIVQLNESVEINCTRENNTRRSIHIGPGRAFYTATGEIIG 321
Qy 303 NTRQAHNCNIRAQWNNNTLOQIATTLREQFGNKTTIAFNQSSGGDPEIVMHSFNCGGFFFC 362
Db 322 DIRQAHNCNLSSTKWNNTLKQIVTKLREHF-NKTIIVFNHSSGGDPEIVMHSFNCGGFFFC 380
Qy 363 NSTQLFNSAWNVTSGTWSVTRKQKDTGDIITLPCRKIKOIINRWQVVGKAMVALPIKGLI 422
Db 381 NITPLFNSTWNYTY--TWNTGSDNTGRNITLQCHIKOIINWQEVGKAMVAPPYRGQI 438
Qy 423 RCSSNITGLLLTRDGGGENQTTETPRPGGDMRDNRSELYKYKVKIIEPLGVAPTKAKR 482
Db 439 RCSSNITGLLLTRD-GGNNSETEIFRPGGDMRDNRSELYKYKVKIIEPLGVAPTKAKR 497
Qy 483 RVVQREKRAVGMFLGAMFLGLGAGSTMGATSWALTVOARQLLSGLVQOONLLRAIKAQ 542
Db 498 RVWQREKRAVG-IGAVFLGLGAGSTMGAASTVTLTVQARLLLSGLVQOONLLRAIEAE 556
Qy 543 QHLLQLTVWGIKQOLQARILAVERYLKDQQLLGIWCGSGKLICTTAVPWNASWNSKSLDKI 602
Db 557 QHLLQLTVWGIKQOLQARVLAVERYLKDQQLLGIWCGSGKLICTTAVPWNASWNSKSLDKI 616
Qy 603 WNNMTWMEWDREIDNYTHLYTLEESQOQKNOQELLDKWSL 649
Db 617 WDNMTWMEWEREIDNYTSLIYSLIEESQOQKNEQELLELDKWSL 663

RESULT 6
US-08-022-835-6
; Sequence 6, Application US/08022835
; Patent No. 5420030
; GENERAL INFORMATION:
; APPLICANT: Reitz Jr., Marvin S.
; APPLICANT: Franchini, Genoveffa
; APPLICANT: Markham, Phillip D.
; APPLICANT: Gallo, Robert C.
; APPLICANT: Lori, Franco C.
; APPLICANT: Popovic, Mikulas
; APPLICANT: Garner, Suzanne
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,835
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-022-835-6

Query Match      81.6%; Score 2834; DB 1; Length 855;
Best Local Similarity 82.2%; Pred. No. 1.9e-225;
Matches 534; Conservative 45; Mismatches 53; Indels 18; Gaps 6;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVVLENVTENF 62
Db 33 LWTVYGVVPWKAEATTLFCASDRKAYDTBVHNVWATHACVPTDNPQEVVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLN--TN-NTNNTLSIIV 119
Db 93 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLRNATNGNDTNTSSRGV 152
Qy 120 WEQKGEKEMRCSFNITTSIRKDVOREVALFYKLDVEPIDDKNTTNTKYRLINCVTSV 179
Db 153 ----GGEMKNCNFNITNIRGVQKVALFYKLDIADIDNN-----SNRRLISCVTSV 204
Qy 180 ITOACPKVSPPIPIHYCTPTGFALLKCNKDKFNGTGTCTNVSTVQCTHGIRPVVSTQLL 239
Db 205 ITOACPKVSPPIPIHYCAPAGFAILCKDKKFGKGTCTNVSTVQCTHGIRPVVSTQLL 264
Qy 240 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 265 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKSHIIGRAFYTTGE 324
Qy 300 ILGNIROAHCHNISRAQWNTLQIATTLREQFGNKTIAPNOSGSGDPEIVHVSFNCGEF 359
Db 325 IIGDIROAHCHNLSRAKWNLTINKIVIKLREQFGNKTIIVFKHSSGSDPEIVHVSFNCGEF 384
Qy 360 FYCNSSTOLFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIK 419
Db 385 FYCNSSTOLFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIR 438
Qy 420 GLIRCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNWRSELYKYKVKIEPLGVAPTK 479
Db 439 GOIRCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNWRSELYKYKVKIEPLGVAPTK 498
Qy 480 AKRVRVQREKAVGMLGAMFLGFLGAAGSTWGTATSMALTVQAROLLGSGIVQOQNLLRAI 539
Db 499 AKRVRVQREKAVG-IGAVFLGFLGAAGSTWGAAMTLTVQAROLLGSGIVQOQNLLRAI 557
Qy 540 KAOQHLLQLTWGIKQLQARILAVERYLKQOQLLGFWGCCKLICTTAVPWNASWSNKTLL 599
Db 558 EAOQHLLQLTWGIKQLQARILAVERYLKQOQLLGFWGCCKLICTTAVPWNASWSNKTLL 617

RESULT 7
US-08-388-809-6
; Sequence 6, Application US/08388809
; Patent No. 5576000
; GENERAL INFORMATION:
; APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
; APPLICANT: GENOVEFFA, MARKHAM, PHILIP D. GALLO, ROBERT
; APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
; APPLICANT: GARTNER, SUZANNE
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK, 3.5"
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,809
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,835
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: LESLIE A. SERUNIAN
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4092US2
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-388-809-6

Query Match      81.6%; Score 2834; DB 1; Length 855;
Best Local Similarity 82.2%; Pred. No. 1.9e-225;
Matches 534; Conservative 45; Mismatches 53; Indels 18; Gaps 6;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVVLENVTENF 62
Db 33 LWTVYGVVPWKAEATTLFCASDRKAYDTBVHNVWATHACVPTDNPQEVVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLN--TN-NTNNTLSIIV 119
Db 93 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLRNATNGNDTNTSSRGV 152
Qy 120 WEQKGEKEMRCSFNITTSIRKDVOREVALFYKLDVEPIDDKNTTNTKYRLINCVTSV 179
Db 153 ----GGEMKNCNFNITNIRGVQKVALFYKLDIADIDNN-----SNRRLISCVTSV 204
Qy 180 ITOACPKVSPPIPIHYCTPTGFALLKCNKDKFNGTGTCTNVSTVQCTHGIRPVVSTQLL 239
Db 205 ITOACPKVSPPIPIHYCAPAGFAILCKDKKFGKGTCTNVSTVQCTHGIRPVVSTQLL 264
Qy 240 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 265 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKSHIIGRAFYTTGE 324
Qy 300 ILGNIROAHCHNISRAQWNTLQIATTLREQFGNKTIAPNOSGSGDPEIVHVSFNCGEF 359
Db 325 IIGDIROAHCHNLSRAKWNLTINKIVIKLREQFGNKTIIVFKHSSGSDPEIVHVSFNCGEF 384
Qy 360 FYCNSSTOLFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIK 419
Db 385 FYCNSSTOLFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIR 438
Qy 420 GLIRCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNWRSELYKYKVKIEPLGVAPTK 479
Db 439 GOIRCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNWRSELYKYKVKIEPLGVAPTK 498
Qy 480 AKRVRVQREKAVGMLGAMFLGFLGAAGSTWGTATSMALTVQAROLLGSGIVQOQNLLRAI 539
Db 499 AKRVRVQREKAVG-IGAVFLGFLGAAGSTWGAAMTLTVQAROLLGSGIVQOQNLLRAI 557
Qy 540 KAOQHLLQLTWGIKQLQARILAVERYLKQOQLLGFWGCCKLICTTAVPWNASWSNKTLL 599
Db 558 EAOQHLLQLTWGIKQLQARILAVERYLKQOQLLGFWGCCKLICTTAVPWNASWSNKTLL 617

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Db 172 ACPKISPEPIPIHYCAPAGPAILKCKNDKTFNGKGPCKNVSVTQCTHGIRPVVSTQLLNG 231
Qy 243 SLAEVVRIRSENFNNAKTIIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 232 SLAEVVRIRSDNFNNAKTIIIVQLKESVEINCTRPNNHTRKSHIGPRAFYTTGELG 291
Qy 303 NIRAHCNISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIIVHNSFNCGEFFYC 362
Db 292 DIRAHCNISRAKWNNTLQIKVILREQFENKTIIVFNHSGDDPEIIVHNSFNCGEFFYC 351
Qy 363 NSTOLFNSAMVNTSGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPILKGLI 422
Db 352 NSTOLFNSAMVNTSGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPILKGLI 405
Qy 423 RCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNWSELYKYKVKIEPLGVAPTAKR 482
Db 406 RCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNWSELYKYKVKIEPLGVAPTAKR 465
Qy 483 RVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIIVQOQNNLLRAIKAO 542
Db 466 RVQREKAVG-IGAVFLGFGAAGSTMGATSMALTVOARQLLSGIIVQOQNNLLRAIKAO 524
Qy 543 QHLLQTLVWGIKQIARILAVERYLKQOQLLGFWGCSGKLICTTAVPWNASWSNKTLDQI 602
Db 525 QRLQTLVWGIKQIARILAVERYLKQOQLLGFWGCSGKLICTTAVPWNASWSNKTLDQI 584
Qy 603 WNNMTWMDREIDNYTHLYTLIEESQOQKQELLDKQWASL 649
Db 585 WNNMTWMDREIDNYTHLYTLIEESQOQKQELLDKQWASL 631

RESULT 10

US-07-956-483-14
; Sequence 14, Application US/07956483
; Patent No. 6261799
; GENERAL INFORMATION:
; APPLICANT: KIENY, Marie-Paule
; TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
; TITLE OF INVENTION: SP160 VARIANT
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,483
; FILING DATE: 31-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/19742
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 05392
; FILING DATE: 02-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feuty, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 017753-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-956-483-14
Query Match 81.1%; Score 2818; DB 2; Length 855;
Best Local Similarity 81.3%; Pred. No. 4e-224;
Matches 534; Conservative 39; Mismatches 54; Indels 30; Gaps 7;
Qy 3 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 33 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 92
Qy 63 NMWKNNVQEHEDIISLWQSLKPCVKLPLCVTLNCTDLNNTNTNTTSLIIVVWEQ 122
Db 93 NMWKNNVQEHEDIISLWQSLKPCVKLPLCVTLNCTDLNNTNTNTTSLIIVVWEQ 148
Qy 123 RGK---GEMRNCNSNITTSIRSKVQREYALFYKLDVEPIDDKNTYNTKRYLNCNTSV 179
Db 149 RGMGEGEMTNCNSNITTSIRSKVQREYALFYKLDVEPIDDKNTYNTKRYLNCNTSV 201
Qy 180 ITOACPKVSEPIPIHYCTPTGFAKLCNDKNGTGTCTNVSTVQCTHGIRPVVSTOLL 239
Db 202 ITOACPKVSEPIPIHYCA-RWFAIINCNNKNGTGTCTNVSTVQCTHGIRPVVSTOLL 260
Qy 240 LNSLAEEVVRSENFNNAKTIIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 261 LNSLAEEVVRSENFNNAKTIIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 320
Qy 300 ILGNIROAHCNISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIIVHNSFNCGEF 359
Db 321 IIGDIRAHCNISRAKWNNTLQIKVILREQFENKTIIFNRSSGDDPEIIVHNSFNCGEF 380
Qy 360 FYCNSSTOLFNSAMVNT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPALP 417
Db 381 FYCNSSTOLFNSAMVNT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPALP 432
Qy 418 IKGLIRCSSNITGLLTRDGG-NGENOTTEIFRPGGDMRDNWSELYKYKVKIEP 472
Db 433 IKGLIRCSSNITGLLTRDGG-NGENOTTEIFRPGGDMRDNWSELYKYKVKIEP 492
Qy 473 LGVAPTAKRVVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIIVQOQ 532
Db 493 LGVAPTAKRVVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIIVQOQ 552
Qy 533 NNLRAIKAOQHLLQTLVWGIKQIARILAVERYLKQOQLLGFWGCSGKLICTTAVPWN 592
Db 553 NNLRAIKAOQHLLQTLVWGIKQIARILAVERYLKQOQLLGFWGCSGKLICTTAVPWN 612
Qy 593 SWSNKTLDQIWNNTWMDREIDNYTHLYTLIEESQOQKQELLDKQWASL 649
Db 613 SWSNKTLDQIWNNTWMDREIDNYTHLYTLIEESQOQKQELLDKQWASL 669
RESULT 11
US-08-375-510-2
; Sequence 2, Application US/08375510
; Patent No. 5576421
; GENERAL INFORMATION:
; APPLICANT: Saito, Atsushi
; APPLICANT: Sinagawa, Hideo
; APPLICANT: Nakata, Atsuo
; TITLE OF INVENTION: HIV ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

Db 174 ACPKVSFEPIPIHYCAPAGFAILKCNKNTFNGTGTCTVSTVQCTHGRPVVSTOLLNG 233
Qy 243 SLAEEVWVRSNFTNNAKTIIVQLNVSVINCTRPNNHTRK--RVTLGPRGVWVTTGEI 300
Db 234 SLAEEVWVRSNFTNNAKTIIVQLNVSVINCTRPNNHTRKSIIRIQPGRAFVTIGKI 321
Qy 301 LGNIROAHCHNISRACNNNTLOQIATTLREOFG-NKTIAFNOSGGDPPIVHVSFNCGGEF 359
Db 294 -GNMQAHCHNISRACNNNTLOQIATTLREOFG-NKTIAFNOSGGDPPIVHVSFNCGGEF 352
Qy 360 FYCNSTOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRILQIINRWQVGVKAMALPI 418
Db 353 FYCNSTOLFNSW---FNSWTSTEGSNNTGSDTITLPCRILQIINRWQVGVKAMALPI 409
Qy 419 KGLRCSNNTITGLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 478
Db 410 SGQIRCSNNTITGLLTRDGGGNGNGSEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 469
Qy 479 KAKRVVOREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGI VQQNNLLRA 538
Db 470 KAKRVVOREKRAVG-IGALFLGFLGAAGSTMGCTSMTLTVOARQLLSDI VQQNNLLRA 528
Qy 539 IKAQHLLQLTVMGILKQIARILAVERYLKQQLLGFWGCCKLICCTTAVPWNASWSNKT 598
Db 529 IEAQHLLQLTVMGILKQIARILAVERYLKQQLLGFWGCCKLICCTTAVPWNASWSNKS 588
Qy 599 LDQIWNMTWMEWDREINNYTHLYTLIESQNOQKQQLLQDKWASL 649
Db 589 LEQIWNMTWMEWDREINNYTHLYTLIESQNOQKQQLLQDKWASL 639

RESULT 13

US-09-309-572-23
; Sequence 23, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; PRIOR FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-309-572-23

Query Match 81.0%; Score 2814.5; DB 2; Length 854;
Best Local Similarity 82.9%; Pred. No. 7.8e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;
Qy 3 LWTVYGVVPWKATTTLCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF 62
Db 34 LWTVYGVVPWKATTTLCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF 93
Qy 63 NMWKNMVQEHEDIISLWDSQKPCVKLTPLCVLTNCTDLNTNTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVQEHEDIISLWDSQKPCVKLTPLCVLTNCTDLNTNTNTSSGRIME- 150
Qy 123 RGKEMRNCNFTITSIRDKVOREVALFYKLDVPEIDNKNNTNTKYLINCNMTSVITQ 182
Db 151 --KGEIKNCNFTISIRDKVQKEYAFYKLDIVPID-----NTSYRLISCNMTSVITQ 201
Qy 183 ACPKVSFEPIPIHYCTPTGFAILLKCNKNGTGTCTVSTVQCTHGRPVVSTOLLNG 242
Db 202 ACPKVSFEPIPIHYCAPAGFAILKCNKNTFNGTGTCTVSTVQCTHGRPVVSTOLLNG 261

Qy 243 SLAEEVWVRSNFTNNAKTIIVQLNVSVINCTRPNNHTRK--RVTLGPRGVWVTTGEI 300
Db 262 SLAEEVWVRSNFTNNAKTIIVQLNVSVINCTRPNNHTRKSIIRIQPGRAFVTIGKI 321
Qy 301 LGNIROAHCHNISRACNNNTLOQIATTLREOFG-NKTIAFNOSGGDPPIVHVSFNCGGEF 359
Db 322 -GNMQAHCHNISRACNNNTLOQIATTLREOFG-NKTIAFNOSGGDPPIVHVSFNCGGEF 380
Qy 360 FYCNSTOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRILQIINRWQVGVKAMALPI 418
Db 381 FYCNSTOLFNSW---FNSWTSTEGSNNTGSDTITLPCRILQIINRWQVGVKAMALPI 437
Qy 419 KGLRCSNNTITGLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 478
Db 438 SGQIRCSNNTITGLLTRDGGGNGNGSEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 497
Qy 479 KAKRVVOREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGI VQQNNLLRA 538
Db 498 KAKRVVOREKRAVG-IGALFLGFLGAAGSTMGCTSMTLTVOARQLLSDI VQQNNLLRA 556
Qy 539 IKAQHLLQLTVMGILKQIARILAVERYLKQQLLGFWGCCKLICCTTAVPWNASWSNKT 598
Db 557 IEAQHLLQLTVMGILKQIARILAVERYLKQQLLGFWGCCKLICCTTAVPWNASWSNKS 616
Qy 599 LDQIWNMTWMEWDREINNYTHLYTLIESQNOQKQQLLQDKWASL 649
Db 617 LEQIWNMTWMEWDREINNYTHLYTLIESQNOQKQQLLQDKWASL 667

RESULT 14

US-09-718-096-23
; Sequence 23, Application US/09718096
; Patent No. 6589763
; GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-718-096-23

Query Match 81.0%; Score 2814.5; DB 2; Length 854;
Best Local Similarity 82.9%; Pred. No. 7.8e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;
Qy 3 LWTVYGVVPWKATTTLCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF 62
Db 34 LWTVYGVVPWKATTTLCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF 93
Qy 63 NMWKNMVQEHEDIISLWDSQKPCVKLTPLCVLTNCTDLNTNTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVQEHEDIISLWDSQKPCVKLTPLCVLTNCTDLNTNTNTSSGRIME- 150
Qy 123 RGKEMRNCNFTITSIRDKVOREVALFYKLDVPEIDNKNNTNTKYLINCNMTSVITQ 182
Db 151 --KGEIKNCNFTISIRDKVQKEYAFYKLDIVPID-----NTSYRLISCNMTSVITQ 201
Qy 183 ACPKVSFEPIPIHYCTPTGFAILLKCNKNGTGTCTVSTVQCTHGRPVVSTOLLNG 242

Db 202 ACPKVSPEPIPIHYCAPAGFAILKCNKNTFNGTGTCTNVTQCTHGIKIRPVVSTQLLLNG 261
Qy 243 SLAEVVIRSENFTNNAKTIIVOLNVSVEINCTRPNNHTRK--RVTLGPRVYVYTTGEI 300
Db 262 SLAEEDVIRSANFTDNAKTIIVOLNVSVEINCTRPNNHTRKSIIRIQRGFGRAFVTIGKI 321
Qy 301 LGNIROAHCNISRAQWNTTLOQIATTLREQFG-NKTIAFNQSSGGDPEIIVMHSFNCGGEF 359
Db 322 -GNMROAHCNISRAKWNATLKQIASKLREQFGNNTIIFKQSSGGDPEIIVTHSFNCGGEF 380
Qy 360 FYCNSLTQFNSAMVTSNGTWSVTRKQKDTG-DIITLPCRILKQILNRWQVVGKAWALPI 418
Db 381 FYCNSLTQFNSW---FNSTWSTEGSNNTGSDTITLPCRILKQILNRWQVVGKAWAPPI 437
Qy 419 KGLRCSNNTGLLLTRDGGENOTTEIFRPGGDMRDNWRSELYKYKVKIPLGVAPT 478
Db 438 SGQIRCSNNTGLLLTRDGGNNNGSEIFRPGGDMRDNWRSELYKYKVKIPLGVAPT 497
Qy 479 KAKERVVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQONNLLRA 538
Db 498 KAKERVVQREKRAVG-IGALFLGFLGAAGSTMGCTSNLTVOARQLLSGIVQONNLLRA 556
Qy 539 IKAQOHLQLTVWGIKQLOARILAVERYLKQDQLLGFPGWCGSKLICTTAVPMNASMNT 598
Db 557 IEAQOHLQLTVWGIKQLOARILAVERYLKQDQLLGIWCGSKLICTTAVPMNASMNTS 616
Qy 599 LDQIWNMTWMDRETDNYTHLYTLIESONQOEKNOQELLDKWSL 649
Db 617 LEQIWNMTWMDREINNTYSLIHSLEESONQOEKNEQELLELDKWSL 667

RESULT 15

US-08-788-815-7
; Sequence 7, Application US/08788815
; Patent No. 5846546
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: 332 No. 5846546th Lauderdale
; APPLICANT: PO Box 318
; APPLICANT: Memphis, TN 38101-0318
; APPLICANT: United States of America
; APPLICANT: Coleclough, Christopher
; APPLICANT: Owens, Randall J.
; APPLICANT: Slobod, Karen
; TITLE OF INVENTION: PREPARATION AND USE OF VIRAL VECTORS FOR
; TITLE OF INVENTION: MIXED ENVELOPE PROTEIN VACCINES AGAINST HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: 411 HACKENSACK AVENUE
; CITY: HACKENSACK
; STATE: NJ
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,815
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: 1340-1-011CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 880 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-788-815-7
Query Match 81.0%; Score 2814; DB 1; Length 880;
Best Local Similarity 82.1%; Pred. No. 8,9e-224; Indels 18; Gaps 9;
Matches 540; Conservative 39; Mismatches 61;
Qy 3 LWTVVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNQEWLENTENF 62
Db 43 LWTVVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNQEWLENTENF 102
Qy 63 NMKNMNVQOMHEDIISLWDQSLKPCVKLTPLCVLNCNTDL--NTNNTNTTSLSIIVW 120
Db 103 NMKNMNVQOMHEDIISLWDQSLKPCVKLTPLCVLNCNTDL--NTNNTNTTSLSIIVW 158
Qy 121 EQR--GKGEWRNCSFNITTSIRDKVQREYALFYKLDVEPID--DNKNTNTNTKYRLN 176
Db 159 GRNIMEGEIKNCSFNISTISIRGVQKEYAFFYKLDIIPIDKGNDSNDTTSYKFTTSCN 218
Qy 177 TSVITQACPKVSEPIPIHYCTPTGFPALLKCNCKFNGTGTCTNVTQCTHGIKIRPVST 236
Db 219 TSVITQACPKVSEPIPIHYCAPAGFAILKCNKNTFNGTGTCTNVTQCTHGIKIRPVST 278
Qy 237 QLLNGSLAEVEVIRSENFTNNAKTIIVOLNVSVEINCTRPNNHTRK--RVTLGPRVW 294
Db 279 QLLNGSLAEVEVIRSANFTDNAKTIIVQLNQSVBEINCTRPNNHTRKSIIRIQRGFGRAF 338
Qy 295 YTTGETILGNIRQAHCNISRAQWNTTLOQIATTLREQFG-NKTIAFNQSSGGDPEIIVMHSF 353
Db 339 VTIGKILGNMROAHCNISRAKWNATLKQIASKLREQFGNNTIIFKQSSGGDPEIIVTHSF 398
Qy 354 NCGGEFFYCNSTOLFNSAMNVTISNGTWSVTRKQKDTG-DIITLPCRILKQILNRWQVVGKA 412
Db 399 NCGGEFFYCNSTOLFNSW---FNSTWSTKGSNNTGSDTITLPCRILKQILNRWQVVGKA 455
Qy 413 MYALPIKGLIRCSNNTGLLLTRDGG-GENOTTEIFRPGGDMRDNWRSELYKYKVKIE 471
Db 456 MYAPPISGGIIRCSNNTGLLLTRDGGANENNESEIFRPGGDMRDNWRSELYKYKVKIE 515
Qy 472 PLGVAPTAKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQ 531
Db 516 PLGVAPTAKRRVQREKRAVGEIGALFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQ 575
Qy 532 QNNLLRAIKAQOHLQLTVWGIKQLOARILAVERYLKQDQLLGFPGWCGSKLICTTAVPMN 591
Db 576 QNNLLRAIEAQOHLQLTVWGIKQLOARILAVERYLKQDQLLGIWCGSKLICTTAVPMN 635
Qy 592 ASWSNKTLDQIWNMTWMDREIDNYTHLYTLIESONQOEKNOQELLDKWSL 649
Db 636 ASWSNKSLEQIWNMTWMDREINNTYSLIHSLEESONQOEKNEQELLELDKWSL 693

Search completed: March 7, 2006, 17:52:51
Job time : 69.9631 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 211.547 Seconds
(without alignments)
1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 3474

Sequence: 1 ANLWTVYGVVWKEATT.....QNQEKQQLLDKWSL 649

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3474	100.0	868	3	US-09-938-406-1
2	2987	86.0	862	5	US-10-780-507-51
3	2977.5	85.7	883	4	US-10-441-926-2
4	2977.5	85.7	883	4	US-10-441-949-2
5	2977.5	85.7	883	5	US-10-780-507-2
6	2977.5	85.7	883	5	US-10-780-507-121
7	2949	84.9	862	5	US-10-780-507-50
8	2896.5	83.4	852	4	US-10-093-953A-29
9	2883.5	83.0	842	4	US-10-190-435-2
10	2883.5	83.0	842	4	US-10-241-009-2
11	2883.5	83.0	842	4	US-10-190-434B-2
12	2883.5	83.0	842	4	US-10-190-305A-2
13	2883.5	83.0	842	5	US-10-976-619-2
14	2883.5	83.0	847	3	US-09-476-242-2
15	2852	82.1	850	3	US-09-966-931-28
16	2852	82.1	850	4	US-10-459-121-28
17	2827.5	81.4	643	4	US-10-032-162-13
18	2827.5	81.4	643	5	US-10-780-993-13
19	2809.5	80.9	856	3	US-09-476-242-1
20	2809.5	80.9	856	5	US-10-891-825-19
21	2809.5	80.9	857	3	US-09-966-931-30
22	2809.5	80.9	857	4	US-10-459-121-30
23	2807	80.8	848	5	US-10-844-658-1
24	2806.5	80.8	863	5	US-10-634-165-11
25	2795.5	80.5	856	4	US-10-196-515-11
26	2795.5	80.5	856	6	US-11-048-554-11
27	2795	80.5	861	4	US-10-026-741-103

28	2790.5	80.3	643	4	US-10-375-657-7	Sequence 7, Appli
29	2789.5	80.3	667	5	US-10-506-851-4	Sequence 4, Appli
30	2789.5	80.3	853	5	US-10-506-851-2	Sequence 2, Appli
31	2781	80.1	665	3	US-09-966-931-32	Sequence 32, Appli
32	2781	80.1	665	4	US-10-459-121-32	Sequence 32, Appli
33	2771.5	79.8	856	5	US-10-844-658-5	Sequence 5, Appli
34	2757	79.4	726	4	US-10-196-515-3	Sequence 3, Appli
35	2757	79.4	726	6	US-11-048-554-3	Sequence 3, Appli
36	2755	79.3	759	4	US-10-196-515-12	Sequence 12, Appli
37	2755	79.3	759	6	US-11-048-554-12	Sequence 12, Appli
38	2736.5	78.8	849	4	US-10-325-468-15	Sequence 15, Appli
39	2736.5	78.8	855	4	US-10-325-468-25	Sequence 25, Appli
40	2729.5	78.6	849	4	US-10-325-468-32	Sequence 32, Appli
41	2728.5	78.5	619	3	US-09-891-609-4	Sequence 4, Appli
42	2728.5	78.5	646	3	US-09-891-609-2	Sequence 2, Appli
43	2728.5	78.5	849	4	US-10-325-468-29	Sequence 29, Appli
44	2720.5	78.3	625	4	US-10-032-162-17	Sequence 17, Appli
45	2720.5	78.3	625	5	US-10-780-993-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-09-938-406-1
; Sequence 1, Application US/09938406
; Patent No. US20020155120A1
; GENERAL INFORMATION:
; APPLICANT: Lowell, George
; APPLICANT: Vancott, Thomas
; APPLICANT: Birx, Deborah
; TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
; TITLE OF INVENTION: INDUCING MUCOSAL IMMUNITY
; FILE REFERENCE: 40646-20002.10
; CURRENT APPLICATION NUMBER: US/09/938,406
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/214,701
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/US 97/12253
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: US 60/021,687
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Virus HIV-1
US-09-938-406-1

Query Match						100.0%; Score 3474; DB 3; Length 868;
Best Local Similarity						100.0%; Pred. No. 2.8e-266;
Matches 649; Conservative						0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ANLWTVYGVVWKEATT	1	ANLWTVYGVVWKEATT	1	FCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 60
Db	33	ANLWTVYGVVWKEATT	1	FCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 92		
Qy	61	NFNWKNMVEQMHEDI	1	ISLWDSQKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 120		
Db	93	NFNWKNMVEQMHEDI	1	ISLWDSQKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 152		
Qy	121	EORGKGMNCSNIT	1	TSRDKYQREYALFKYLDVEPIDDKNTNTNTRYLINCNTSVI 180		
Db	153	EORGKGMNCSNIT	1	TSRDKYQREYALFKYLDVEPIDDKNTNTNTRYLINCNTSVI 212		
Qy	181	TOACPKVSFPIPIH	1	YCTPTGFPALLKCNDRKFKGTGCTNVSTVQCTHGRPVVSTQLLL 240		
Db	213	TOACPKVSFPIPIH	1	YCTPTGFPALLKCNDRKFKGTGCTNVSTVQCTHGRPVVSTQLLL 272		
Qy	241	NGSLAEVEVIRSE	1	NFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 300		
Db	273	NGSLAEVEVIRSE	1	NFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 332		

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QY 301 LGNIROAHCNISRAQWNNTLQIATTLREQFGNKTIAFNSSGGDPEIVMHSFNCGEFF 360
Db 333 LGNIROAHCNISRAQWNNTLQIATTLREQFGNKTIAFNSSGGDPEIVMHSFNCGEFF 392
QY 361 YCNSTOLFNSAWNVTSGTWSVTRKOKDGTGDIITLPCRILQIINRWQVVGKAMYPKIG 420
Db 393 YCNSTOLFNSAWNVTSGTWSVTRKOKDGTGDIITLPCRILQIINRWQVVGKAMYPKIG 452
QY 421 LIRCSSNITGLLTRDGGGENQTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTGA 480
Db 453 LIRCSSNITGLLTRDGGGENQTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTGA 512
QY 481 KRRVQREKRAVGMGLGFLGAGSTWGATSMALTVOARQLLSGIVQQNNLLRAIK 540
Db 513 KRRVQREKRAVGMGLGFLGAGSTWGATSMALTVOARQLLSGIVQQNNLLRAIK 572
QY 541 AQOHLQLTVMGILKQOARILAVERYLKDOQLLGFWGCSGKLICTTAVPWNASWSNKTLD 600
Db 573 AQOHLQLTVMGILKQOARILAVERYLKDOQLLGFWGCSGKLICTTAVPWNASWSNKTLD 632
QY 601 QIWNMTWMEWDREIDNYTHLIYTLIESQNKQOELLQDKWASL 649
Db 633 QIWNMTWMEWDREIDNYTHLIYTLIESQNKQOELLQDKWASL 681

RESULT 2
US-10-780-507-51
; Sequence 51, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10780, 507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204, 204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183, 659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447, 586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Least squares and minimum of means center of tree reconstruction
; OTHER INFORMATION: of clade B gp 160 protein sequence
US-10-780-507-51

Query Match 86.0%; Score 2987; DB 5; Length 862;
Best Local Similarity 86.6%; Pred. No. 1.1e-227;
Matches 563; Conservative 31; Mismatches 46; Indels 10; Gaps 6;
QY 3 LWTVVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF 62
Db 33 LWTVVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF 92
QY 63 NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVWSEQ 122
Db 93 NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLN-KNATNTSSS-----GEM 147
QY 123 RGKGMNRCSFNITTSIRDVKQREYALFYKLDVEPIDDKNKTNTNTKYLINCNSTSVITQ 182
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Db 148 MEKGEIKNCSFNITTSIRDVKQREYALFYKLDVVPIDNDNNTNTTTSYRLISCNSTSVITQ 207
QY 183 ACPKVSFEPIPIHYCTPTGTFALLKNDKKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG 242
Db 208 ACPKVSFEPIPIHYCAPAGFAILKNDKKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG 267
QY 243 SLAEAEVWIRSNFTNNAKTIIVQLNVSVEINCTRENNHTRKRVTLTGPGRVWYTTGEILG 302
Db 268 SLAEAEVWIRSNFTNNAKTIIVQLNVSVEINCTRENNHTRKSIHIGPGRFAFTTGEIIG 327
QY 303 NTRQAHCNISRAQWNNTLQIATTLREQFG-NKTIAFNOSGGDPEIVMHSFNCGEFFY 361
Db 328 DIRQAHCNISRAQWNNTLQIIVKILREQFGNNKTIIVFNQSSGGDPEIVMHSFNCGEFFY 387
QY 362 CNSTOLFNSAWNVTSGTWSVTRKOKDT-GDIITLPCRILQIINRWQVVGKAMYPKIG 420
Db 388 CNSTOLFNSWTNGT--WTWNTTEGSDNTEGDTITLPCRILQIINRWQVVGKAMYPKIG 445
QY 421 LIRCSSNITGLLTRDGGGEN-QTTETFRPGGDMRDNRSELYKYKVKIEPLGVAPTGA 479
Db 446 QIRCSSNITGLLTRDGGNNNTNETEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTGA 505
QY 480 AKRRVVQREKRAVGMGLGAGSTWGATSMALTVOARQLLSGIVQQNNLLRAI 539
Db 506 AKRRVVQREKRAVGIITGAVFLGAGSTMGAAASMTLTVOARQLLSGIVQQNNLLRAI 565
QY 540 KAOHLQLTVMGILKQOARILAVERYLKDOQLLGFWGCSGKLICTTAVPWNASWSNKTLD 599
Db 566 EAQOHLQLTVMGILKQOARILAVERYLKDOQLLGFWGCSGKLICTTAVPWNASWSNKTLD 625
QY 600 DOIWNMTWMEWDREIDNYTHLIYTLIESQNKQOELLQDKWASL 649
Db 626 DOIWNMTWMEWDREIDNYTHLIYTLIESQNKQOELLQDKWASL 675

RESULT 3
US-10-441-926-2
; Sequence 2, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-011001
; CURRENT APPLICATION NUMBER: US/10/441, 926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183, 659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide
US-10-441-926-2

Query Match 85.7%; Score 2977.5; DB 4; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;
QY 3 LWTVVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF 62
Db 33 LWTVVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF 92
QY 63 NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVWSEQ 122
Db 93 NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNRTATNTNTSSATNTTTS 152
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; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence
US-10-780-507-2

Query Match      85.7%; Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

Qy 3 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 33 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 63 NMKNMNVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 122
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 93 NMKNMNVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 152
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 123 RG-----KGMNRCNFNITTSIRDKVQREYALFYKLDVEPID-DNKNTNTTKYRLIN 174
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 153 SGGTMEGEKGEIKNCSFNVTTSIRDKQKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 175 CNTSVITQACPKVSFEPPIHYCTPTGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 234
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 213 CNTSVITQACPKVSFEPPIHYCTPAGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 272
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 235 STOLLNGSLAEEVVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVW 294
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 273 STOLLNGSLAEEVVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKSIPIGPRAL 332
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 295 YTTGEILGNIRQAHCNISRAQWNTLQOIATTLREOFGNK--TIAFNQSSGGDPEIVMHS 352
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 333 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVMHS 392
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 353 FNCGGFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 407
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 393 FNCGGFFYCNSTOLFNSWHP--NGTWGNNTNRSNNAADDNDTITLPCRKQIINRWQ 450
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 408 VVGKAMYPALPKGLIRCSSNITGLLLTRDGGGNGT-----TEIFRPGGDMRDNRSELY 463
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 451 EVGKAMYPALPKGLIRCSSNITGLLLTRDGGGNGNTNTDTEIFRPGGDMRDNRSELY 510
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 464 KYKVKIIEPLGVAPTAKRVVQREKAVGMGLGFLGAGSTMGATSMALTVOARQ 523
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 511 KYKVKIIEPLGVAPTAKRVVQREKAVGMGLGFLGAGSTMGAASTMTLTVQARQ 570
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 524 LLSGIVQOQNLLRAIKAOQHLLQLTWGIKQLQARILAVERYLKDQQLLGFWGCSSGKLI 583
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 571 LLSGIVQOQNLLRAIEAQHLLQLTWGIKQLQARVLAVERYLKDQQLLGFWGCSSGKLI 630
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 584 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQKQELLQ 643
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 631 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQKQELLQ 690
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 644 DKWASL 649
Db | | | | |
Qy 691 DKWASL 696
Db | | | | |

RESULT 6
US-10-780-507-121
; Sequence 121, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
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; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
US-10-780-507-121
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Query Match      85.7%; Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

Qy 3 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 33 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 63 NMKNMNVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 122
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 93 NMKNMNVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 152
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 123 RG-----KGMNRCNFNITTSIRDKVQREYALFYKLDVEPID-DNKNTNTTKYRLIN 174
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 153 SGGTMEGEKGEIKNCSFNVTTSIRDKQKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 175 CNTSVITQACPKVSFEPPIHYCTPTGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 234
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 213 CNTSVITQACPKVSFEPPIHYCTPAGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 272
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 235 STOLLNGSLAEEVVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVW 294
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 273 STOLLNGSLAEEVVIRSENFNTNAKTIIVQLNVSVVEINCTRPNNHTRKSIPIGPRAL 332
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 295 YTTGEILGNIRQAHCNISRAQWNTLQOIATTLREOFGNK--TIAFNQSSGGDPEIVMHS 352
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 333 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVMHS 392
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 353 FNCGGFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 407
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 393 FNCGGFFYCNSTOLFNSWHP--NGTWGNNTNRSNNAADDNDTITLPCRKQIINRWQ 450
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 408 VVGKAMYPALPKGLIRCSSNITGLLLTRDGGGNGT-----TEIFRPGGDMRDNRSELY 463
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 451 EVGKAMYPALPKGLIRCSSNITGLLLTRDGGGNGNTNTDTEIFRPGGDMRDNRSELY 510
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 464 KYKVKIIEPLGVAPTAKRVVQREKAVGMGLGFLGAGSTMGATSMALTVOARQ 523
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 511 KYKVKIIEPLGVAPTAKRVVQREKAVGMGLGFLGAGSTMGAASTMTLTVQARQ 570
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 524 LLSGIVQOQNLLRAIKAOQHLLQLTWGIKQLQARILAVERYLKDQQLLGFWGCSSGKLI 583
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 571 LLSGIVQOQNLLRAIEAQHLLQLTWGIKQLQARVLAVERYLKDQQLLGFWGCSSGKLI 630
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 584 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQKQELLQ 643
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 631 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQKQELLQ 690
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 644 DKWASL 649
Db | | | | |
Qy 691 DKWASL 696
Db | | | | |
```

RESULT 7
US-10-780-507-50
; Sequence 50, Application US/10780507
; Publication No. US2005013787A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: Li, Fusheng
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 50
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Most recent common ancestor reconstruction of clade B gp 160 prot
; OTHER INFORMATION: ein sequence
US-10-780-507-50

Query Match 84.9%; Score 2949; DB 5; Length 862;
Best Local Similarity 85.6%; Pred. No. 1.1e-224; Mismatches 52; Indels 10; Gaps 6;
Matches 557; Conservative 32

Qy 2 NLWTVVYGVVPVKEATTTLCASDAKAYDEAHNHWATHACVPTNPQEVLENVTEN 61
Db 32 NLWTVVYGVVPVKEATTTLCASDAKAYDEAHNHWATHACVPTNPQEVLENVTEN 91
Qy 62 FNMKNMNVQMHEDIISLWDQSLKPCVKLPCLVTLNCTDLNNTNTNTTSLIIVWE 121
Db 92 FNMKNMNVQMHEDIISLWDQSLKPCVKLPCLVTLNCTDLNNTNTNTTSLIIVWE 146
Qy 122 QRGKGMKNCNFNTTIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVIT 181
Db 147 TMRGEMKNCNFNTTIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVIT 206
Qy 182 QACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGIRPVWSTQLLN 241
Db 207 QACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCKNVSTVCTGIRPVWSTQLLN 266
Qy 242 GSIAEEVVRSENFTNNAKTIIVQLNVSVBEINCTRPNNHTRKRVTLGPGRWYTTGEIL 301
Db 267 GSIAEEVVRSENFTNNAKTIIVQLNVSVBEINCTRPNNHTRKRVTLGPGRWYTTGEII 326
Qy 302 GNIQAHCNISRAQWNNTLOIATILRBQFG-NKTIAPNQSGGDPPEIVMHSFNCGGEFF 360
Db 327 GDIRQAHCNISRAKWNNTLKQVVTKLREQFGNNKTIIVFNPSGGDPPEIVMHSFNCGGEFF 386
Qy 361 YCNSQLPNSAWNTSNTGWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMVALPIKG 420
Db 387 YCNTIQLFNSWNST-EGSNNTGSGNTTILPCRIKQIINRWQVGVKAMVALPIRG 445
Qy 421 LIRCSSNITGLLTRDGGENQOT--TEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 478
Db 446 QIKCSSNITGLLTRD--GGENSTNETEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 504
Qy 479 KAKRRVVQREKRAVGMGLGAMFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQNNLLRA 538

Db 505 KAKRRVVQREKRAVGMGLGAMFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQNNLLRA 564
Qy 539 IKAQHLLQLTVMGIKOLQARILAVERYLKQQLLGFWGSGCKLICCTAVPWNASWSNKT 598
Db 565 IEAQHLLQLTVMGIKOLQARVLAVERYLRDQQLLGFWGSGCKLICCTAVPWNASWSNKS 624
Qy 599 LDQIWNNTWMEWDREIDNTHTLIYTLIESQNOEKNOQELQLDQKWSL 649
Db 625 LDKIWNNTWMEWDREIDNTHTLIYTLIESQNOEKNOQELQLDQKWSL 675

RESULT 8
US-10-093-953A-29
; Sequence 29, Application US/10093953A
; Publication No. US20040105871A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Smith, James M.
; APPLICANT: Hua, Jian
; APPLICANT: Moss, Bernard
; APPLICANT: Amara, Rama
; APPLICANT: Wyatt, Linda
; APPLICANT: Earl, Patricia
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
; TITLE OF INVENTION: AN IMMUNE RESPONSE
; FILE REFERENCE: 12804-005002
; CURRENT APPLICATION NUMBER: US/10/093,953A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/798,675
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US01/06795
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/324,845
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/325,004
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein encoded by construct of vaccine vector
; OTHER INFORMATION: pGA2 and insert JS2 expressing clade HIV-1 VL
US-10-093-953A-29

Query Match 83.4%; Score 2896.5; DB 4; Length 852;
Best Local Similarity 83.6%; Pred. No. 1.6e-220; Mismatches 40; Indels 19; Gaps 6;
Matches 544; Conservative 40

Qy 2 NLWTVVYGVVPVKEATTTLCASDAKAYDEAHNHWATHACVPTNPQEVLENVTEN 61
Db 32 NLWTVVYGVVPVKEATTTLCASDAKAYDEAHNHWATHACVPTNPQEVLENVTEN 91
Qy 62 FNMKNMNVQMHEDIISLWDQSLKPCVKLPCLVTLNCTDLNNTNTNTTSLIIVW 120
Db 92 FNMKNMNVQMHEDIISLWDQSLKPCVKLPCLVTLNCTDLNNTNTNTTSLIIVW 144
Qy 121 EQRGKGMKNCNFNTTIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVI 180
Db 145 --GMRGKNCNFNTTIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVI 197
Qy 181 TOACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGIRPVWSTQLLN 240
Db 198 TOACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCKNVSTVCTGIRPVWSTQLLN 257
Qy 241 NGSIAEEVVRSENFTNNAKTIIVQLNVSVBEINCTRPNNHTRKRVTLGPGRWYTTGEI 300

Db 258 NGLAEVEVIRSNFTDNNKIIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTGTGEI 317
Qy 301 LGNIROAHCNISRAQNNNTLQIATTLREQFG-NKTIAFNOSGGDDEIIVMHSFNCGGEF 359
Db 318 IGDIRQAHCNISRTKWNNTLNQIATLKEQGNKNTIVFQSSGGDDEIIVMHSFNCGGEF 377
Qy 360 FYCNSTOLFNSAMVNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI 418
Db 378 FYCNSTOLFNSWTF--NGTWLNTQSGTGTEDTITLPCRIKQIINRWQVVGKAMYAPPI 435
Qy 419 KGLIRCSSNITGLLLTRDGGGENTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 478
Db 436 RGQIRCSSNITGLLLTRDGGTSSGSEIFRPGGDMRDNWRSELYKYKVKVIEPLGVAPT 495
Qy 479 KAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLLRA 538
Db 496 KAKRVVQREKRAVGTIGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLLRA 555
Qy 539 IKAQOHLQLTVMGIKOLARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKT 598
Db 556 IEAQOHLQLTVMGIKOLARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKT 615
Qy 599 LDQIWNMTWMDREIDNTHLYTLIESONQOQKNOQELLQDKWASL 649
Db 616 LDWIWDMTWMEWEREIDNTHLYTLIESONQOQKNOQELLQDKWASL 666

RESULT 9
US-10-190-435-2
; Sequence 2, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SF162
US-10-190-435-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 28 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 87
Qy 63 NMKNKNNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 88 NMKNKNNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTKSSN-----WKE 141
Qy 123 RGKGMNRCFNITTSIRDQVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNSTVITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEYALFYKLDVVPIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSFEPIPIHYCTPTGTFALLKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 197 ACPKVSFEPIPIHYCAPAGFAILKCNDDKFGNGSGPCTNVSTVQCTHGIRPVVSTQLLNG 256
Qy 243 SLAEVEVIRSNFTNNAKIIIVQLNVSVINCTRPNNNTRKVTILGPGRVWVTTGELLG 302

Db 257 SLAEVEVIRSNFTDNNKIIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTGTGEI 316
Qy 303 NIOAHCNISRQNNNTLQIATTLREQFGNKTIAFNOSGGDDEIIVMHSFNCGGEFYC 362
Db 317 DIRQAHCNISGEKNNNTLQIATTLREQFGNKTIVFQSSGGDDEIIVMHSFNCGGEFYC 376
Qy 363 NSTOLFNSAMVNT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALP 417
Db 377 NSTOLFNSWNTNIGPNTNGT-----ITLPCRIKQIINRWQVVGKAMYAPP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGE-NOTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVA 476
Db 424 IRQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGDMRDNWRSELYKYKVKVIEPLGVA 483
Qy 477 PTAKRRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLL 536
Db 484 PTAKRRVVQREKRAV--TLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLL 542
Qy 537 RAIKAQOHLQLTVMGIKOLARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSN 596
Db 543 RAIKAQOHLQLTVMGIKOLARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSN 602
Qy 597 KTLDOQIWNMTWMDREIDNTHLYTLIESONQOQKNOQELLQDKWASL 649
Db 603 KSLDQIWNMTWMEWEREIDNTHLYTLIESONQOQKNOQELLQDKWASL 655

RESULT 10
US-10-241-009-2
; Sequence 2, Application US/10241009
; Publication No. US20030170614A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.21
; CURRENT APPLICATION NUMBER: US/10/241,009
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SF162
US-10-241-009-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 28 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 87
Qy 63 NMKNKNNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 88 NMKNKNNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTKSSN-----WKE 141
Qy 123 RGKGMNRCFNITTSIRDQVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNSTVITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEYALFYKLDVVPIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSFEPIPIHYCTPTGTFALLKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 197 ACPKVSFEPIPIHYCAPAGFAILKCNDDKFGNGSGPCTNVSTVQCTHGIRPVVSTQLLNG 256
Qy 243 SLAEVEVIRSNFTNNAKIIIVQLNVSVINCTRPNNNTRKVTILGPGRVWVTTGELLG 302

Db 257 SLABEGVIRSENFDTNAKTIIVQLKESVEINCTRPNNNTRKSIITIGPGRFYATGDIIG 316
Qy 303 NIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 317 DIROAHCHNISGEKWNNTLKQIVTKLQAOFGNKTIVFKOSSGGDPPEIVMHSFNCGGEFFYC 376
Qy 363 NSTOLFNSAWNVT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAWYALP 417
Db 377 NSTOLFNSAWNVTIGPNNNGT-----ITLPCRIKQIINRWQVVGKAWYAPP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 476
Db 424 IRGQIRCSSNITGLLLTRDGGGEISNTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 483
Qy 477 PTKAKRRVVOREKRAVGMFLGFLGAAGSTWGATSMALTVOARQLLSGIVOOQNLL 536
Db 484 PTKAKRRVVOREKRAV-TLGAMFLGFLGAAGSTWGARSLLTITVOARQLLSGIVOOQNLL 542
Qy 537 RAIKAQOHLQLTWGIIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWN 596
Db 543 RAIKAQOHLQLTWGIIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWN 602
Qy 597 KTLDOINNNMTMEWDREIDNYTHLYTLIESQKQKQOELLQDLKWSL 649
Db 603 KSLDOINNNMTMEWDREIDNYTHLYTLIESQKQKQOELLQDLKWSL 655

RESULT 11

US-10-190-434B-2
; Sequence 2, Application US/10190434B
; Publication No. US20030194800A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/10/190,434B
; CURRENT FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SP162
US-10-190-434B-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWVTYYGVVPWKEATTLFCASDAKAYDTTEAHNVWATHACVPTNPDPQEVLENVTENF 62
Db 28 LWVTYYGVVPWKEATTLFCASDAKAYDTTEAHNVWATHACVPTNPDPQEVLENVTENF 87
Qy 63 NMWKNMVQWQHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 88 NMWKNMVQWQHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTKSN-----WKE 141
Qy 123 RGKEMRNCNFIITTSIRDKVQREYALFYKLDVPEIDNKNNTNTNTKYLINCNTSVITQ 182
Db 142 MDRGEIKNCNCFKVTTSIRNKQKEALFYKLDVPEIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSPEPIPIHYCTPTGFPALLKCNCKKFGTGTCTNVSTVQCTHGRIPVWSTQLLNG 242
Db 197 ACPKVSPEPIPIHYCAPAGFAILKCNCKKFGSGPCTNVSTVQCTHGRIPVWSTQLLNG 256
Qy 243 SLABEEVIRSENFDTNAKTIIVQLKESVEINCTRPNNNTRKSIITIGPGRFYATGDIIG 302
Db 257 SLABEEVIRSENFDTNAKTIIVQLKESVEINCTRPNNNTRKSIITIGPGRFYATGDIIG 316

Qy 303 NIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 317 DIROAHCHNISGEKWNNTLKQIVTKLQAOFGNKTIVFKOSSGGDPPEIVMHSFNCGGEFFYC 376
Qy 363 NSTOLFNSAWNVT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAWYALP 417
Db 377 NSTOLFNSAWNVTIGPNNNGT-----ITLPCRIKQIINRWQVVGKAWYAPP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 476
Db 424 IRGQIRCSSNITGLLLTRDGGGEISNTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 483
Qy 477 PTKAKRRVVOREKRAVGMFLGFLGAAGSTWGATSMALTVOARQLLSGIVOOQNLL 536
Db 484 PTKAKRRVVOREKRAV-TLGAMFLGFLGAAGSTWGARSLLTITVOARQLLSGIVOOQNLL 542
Qy 537 RAIKAQOHLQLTWGIIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWN 596
Db 543 RAIKAQOHLQLTWGIIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWN 602
Qy 597 KTLDOINNNMTMEWDREIDNYTHLYTLIESQKQKQOELLQDLKWSL 649
Db 603 KSLDOINNNMTMEWDREIDNYTHLYTLIESQKQKQOELLQDLKWSL 655

RESULT 12

US-10-190-305A-2
; Sequence 2, Application US/10190305A
; Publication No. US20030198621A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
; FILE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SP162
US-10-190-305A-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWVTYYGVVPWKEATTLFCASDAKAYDTTEAHNVWATHACVPTNPDPQEVLENVTENF 62
Db 28 LWVTYYGVVPWKEATTLFCASDAKAYDTTEAHNVWATHACVPTNPDPQEVLENVTENF 87
Qy 63 NMWKNMVQWQHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 88 NMWKNMVQWQHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTKSN-----WKE 141
Qy 123 RGKEMRNCNFIITTSIRDKVQREYALFYKLDVPEIDNKNNTNTNTKYLINCNTSVITQ 182
Db 142 MDRGEIKNCNCFKVTTSIRNKQKEALFYKLDVPEIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSPEPIPIHYCTPTGFPALLKCNCKKFGTGTCTNVSTVQCTHGRIPVWSTQLLNG 242
Db 197 ACPKVSPEPIPIHYCAPAGFAILKCNCKKFGSGPCTNVSTVQCTHGRIPVWSTQLLNG 256
Qy 243 SLABEEVIRSENFDTNAKTIIVQLKESVEINCTRPNNNTRKSIITIGPGRFYATGDIIG 302
Db 257 SLABEEVIRSENFDTNAKTIIVQLKESVEINCTRPNNNTRKSIITIGPGRFYATGDIIG 316

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 7, 2006, 17:53:05 ; Search time 24.8879 Seconds
(without alignments)
521.549 Million cell updates/sec
Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474
Sequence: 1 ANLWTVYGVVWKEATTT.....ONQEKNOQELLQDKWASL 649
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 135346 seqs, 20000420 residues
Total number of hits satisfying chosen parameters: 135346
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
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7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	2809.5	80.9	856	US-10-510-947-8
2	2809.5	80.9	856	Sequence 8, Appli
3	2809.5	80.9	856	Sequence 13, Appl
4	2756.5	79.3	681	Sequence 1, Appli
5	2756.5	79.3	681	Sequence 25, Appl
6	2668.5	76.8	669	Sequence 27, Appl
7	2668.5	76.8	669	Sequence 29, Appl
8	2509.5	72.2	613	Sequence 31, Appl
9	2509.5	72.2	801	Sequence 35, Appl
10	2489	71.6	854	Sequence 37, Appl
11	2421.5	69.7	601	Sequence 219, App
12	2421.5	69.7	789	Sequence 39, Appl
13	1140	32.8	879	Sequence 340, App
14	1112.5	32.0	860	Sequence 217, App
15	653	18.8	145	Sequence 11, Appl
16	511.5	14.7	379	Sequence 3, Appli
17	436.5	12.6	146	Sequence 10, Appl
18	330.5	9.5	220	Sequence 1, Appli
19	330.5	9.5	225	Sequence 7, Appli
20	330.5	9.5	225	Sequence 8, Appli
21	330.5	9.5	227	Sequence 9, Appli
22	330.5	9.5	267	Sequence 2, Appli
23	316	9.1	213	Sequence 19, Appl
24	275	7.9	151	Sequence 215, App
25	265	7.6	102	Sequence 18, Appl

26	189	5.4	40	7	US-11-151-598-3	Sequence 3, Appli
27	184	5.3	44	7	US-11-187-887-24	Sequence 24, Appl
28	183	5.3	41	7	US-11-107-364-34	Sequence 34, Appl
29	172	5.0	36	7	US-11-151-598-11	Sequence 11, Appl
30	171	4.9	37	6	US-10-841-956A-2	Sequence 2, Appli
31	171	4.9	37	7	US-11-029-003-2	Sequence 2, Appli
32	167	4.8	38	7	US-11-151-598-4	Sequence 4, Appli
33	166	4.8	35	7	US-11-096-725-16	Sequence 16, Appl
34	166	4.8	35	7	US-11-096-725-21	Sequence 21, Appl
35	165	4.7	47	7	US-11-151-598-5	Sequence 5, Appli
36	164	4.7	35	7	US-11-096-725-18	Sequence 18, Appl
37	162	4.7	40	7	US-11-151-598-6	Sequence 6, Appli
38	160	4.6	34	7	US-11-112-277-8	Sequence 8, Appli
39	160	4.6	34	7	US-11-112-277-36	Sequence 36, Appl
40	160	4.6	34	7	US-11-151-598-10	Sequence 10, Appl
41	160	4.6	34	7	US-11-151-598-12	Sequence 12, Appl
42	160	4.6	35	7	US-11-112-277-7	Sequence 7, Appli
43	160	4.5	35	7	US-11-112-277-37	Sequence 37, Appl
44	157	4.5	35	7	US-11-115-425-1	Sequence 1, Appli
45	157	4.5	35	7	US-11-115-425-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-510-947-8
; Sequence 8, Application US/10510947
; Publication No. US20050255123A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Medina, Maria Fe C.
; APPLICANT: Kobinger, Gary
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses, Therefor
; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/385,704
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/427,752
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-510-947-8

Query Match	80.9%	Score	2809.5	DB 6	Length	856			
Best Local Similarity	82.6%	Pred. No.	4.6e-251						
Matches	538	Conservative	38	Mismatches	56	Indels	19	Gaps	9
Qy	3	LWTVYGVVWKEATTTLCASDAKAYDTAAHNVWATHACVPTNPNPQEVVLENVTENF	62						
Db	34	LWTVYGVVWKEATTTLCASDAKAYDTAAHNVWATHACVPTNPNPQEVVLENVTENF	93						
Qy	63	NMKNVQKHEDIIISLWQSLKPCVKLTPLCVTLNCTDLNTNTNTTSLIIVVWQ	122						
Db	94	NMKNVQKHEDIIISLWQSLKPCVKLTPLCVSLKCTDL--KNDTNTSSSGRMIME-	150						
Qy	123	RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDNKNNTNTKYLINCNTSVITQ	182						
Db	151	--KGEIKNCFSNITSIRGVQKEYAFYKLDIIPDN-----DTSYKLTSCNTSVITQ	203						
Qy	183	ACPKVSEPIPIHYCTPTGFAILLKNDKNGTGPCTNVSTVQCTHGIRPVWSTOLLNG	242						
Db	204	ACPKVSEPIPIHYCAPAGFAILLKNDKNGTGPCTNVSTVQCTHGIRPVWSTOLLNG	263						
Qy	243	SLAEYVIRSENFNTNNAKTIIVQLNVSVBEINCTRPNNHTRKRVTL--GPGRVWYTTGEI	300						

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Db 264 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 323
Qy 301 LGNIRQAHNCISRAQWNTLQOIATTLREQFG-NKTIAFNQSOGSDPEIWMHSFNCGGEF 359
Db 324 -GNRQAHNCISRAKWNNTLKQIASLREQFGNKTIIIFKQSSGGDPEIVTHSFNCGGEF 382
Qy 360 FYCNSQLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKIQIINRWQVVGKAMYALPI 418
Db 383 FYCNSQLFNSW--FNSWTSGSNTTGSDDITLPCRKIQIINRWQVVGKAMYAPPI 439
Qy 419 KGLIRCSNITGLLLTRDGGENOTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 478
Db 440 SGQIRCSNITGLLLTRDGGNSNESEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 499
Qy 479 KAKRRVQREKRAVGMFLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 500 KAKRRVQREKRAVG-IGALFLGAGSTMGASMTLTVOARQLLSGIVQOQNLLRA 558
Qy 539 IKAQHLLQLTVWGIKQIARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKT 598
Db 559 IEAQHLLQLTVWGIKQIARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKS 618
Qy 599 LDQIWNMTWMDREIDNYTHLYTILIESQOQEKNOQELLQDKWASL 649
Db 619 LEQIWNHTTWMDREINNYTSLIHSLIESQOQEKNEQELLELDKWASL 669

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RESULT 2

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US-11-042-988-13
; Sequence I3, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 856
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
US-11-042-988-13

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Query Match 80.9%; Score 2809.5; DB 7; Length 856;
Best Local Similarity 82.6%; Pred. No. 4.6e-251;
Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;

Qy 3 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMWKNVQVQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 122
Db 94 NMWKNVQVQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 150
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPDNNKNTNTNTKYRLINCNVTITQ 182
Db 151 --KGEIKNCSFNISTIRGVQKEYAFYKLDIIPDN-----DTSYKLTSCNTSVITQ 203
Qy 183 ACPKVSFEPIPIHYCTPTGFPALLKCNKDFGPGCTNVSTVQCTHGIRPVWSTQLLNG 242
Db 204 ACPKVSFEPIPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 263
Qy 243 ACPKVSFEPIPIHYCTPTGFPALLKCNKDFGPGCTNVSTVQCTHGIRPVWSTQLLNG 300
Db 264 ACPKVSFEPIPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 323
Qy 243 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 300
Db 264 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 323
Qy 243 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 300

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Db 264 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 323
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Db 324 -GNRQAHNCISRAKWNNTLKQIASLREQFGNKTIIIFKQSSGGDPEIVTHSFNCGGEF 382
Qy 360 FYCNSQLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKIQIINRWQVVGKAMYALPI 418
Db 383 FYCNSQLFNSW--FNSWTSGSNTTGSDDITLPCRKIQIINRWQVVGKAMYAPPI 439
Qy 419 KGLIRCSNITGLLLTRDGGENOTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 478
Db 440 SGQIRCSNITGLLLTRDGGNSNESEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 499
Qy 479 KAKRRVQREKRAVGMFLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 500 KAKRRVQREKRAVG-IGALFLGAGSTMGASMTLTVOARQLLSGIVQOQNLLRA 558
Qy 539 IKAQHLLQLTVWGIKQIARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKT 598
Db 559 IEAQHLLQLTVWGIKQIARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKS 618
Qy 599 LDQIWNMTWMDREIDNYTHLYTILIESQOQEKNOQELLQDKWASL 649
Db 619 LEQIWNHTTWMDREINNYTSLIHSLIESQOQEKNEQELLELDKWASL 669

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RESULT 3

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US-11-135-235-1
; Sequence 1, Application US/11135235
; Publication No. US20060019395A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; TITLE OF INVENTION: Lenticral Vectors and Uses Thereof
; FILE REFERENCE: 20363-027
; CURRENT APPLICATION NUMBER: US/11/135,235
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 60/589,610
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 856
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
US-11-135-235-1

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Query Match 80.9%; Score 2809.5; DB 7; Length 856;
Best Local Similarity 82.6%; Pred. No. 4.6e-251;
Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;

Qy 3 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMWKNVQVQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 122
Db 94 NMWKNVQVQWHEHDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 150
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPDNNKNTNTNTKYRLINCNVTITQ 182
Db 151 --KGEIKNCSFNISTIRGVQKEYAFYKLDIIPDN-----DTSYKLTSCNTSVITQ 203
Qy 183 ACPKVSFEPIPIHYCTPTGFPALLKCNKDFGPGCTNVSTVQCTHGIRPVWSTQLLNG 242
Db 204 ACPKVSFEPIPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 263
Qy 243 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 300
Db 264 SLAEVEVIRSVNFTDNTAKTIIIVQLNTSVBEINCTRPNNNTRKRIIRIQRGPGRAFVTIGKI 323
Qy 301 LGNIRQAHNCISRAQWNTLQOIATTLREQFG-NKTIAFNQSOGSDPEIWMHSFNCGGEF 359

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Db 324 -GNMQAHCHNSRAKWNNTLQKIAKLEQFGNNTIIFKQSSGGDPPIVTHSFNCGEF 382
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 Qy 479 KAKRVVQREKRAVGMGLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
 Db 500 KAKRVVQREKRAVG-IGALFLGFLGAAGSTMGASMTLTVOARQLLSGIVQOQNLLRA 558
 Qy 539 IKAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCGSKLICCTTAVPWNASWNT 598
 Db 559 IEAQOHLQLLTWGIKQIARILAVERYLKQOQLLGFPGCGSKLICCTTAVPWNASWNTS 618
 Qy 599 LDOIWNNTWMEWDREIDNTHLYTLIEESONQOEKNOQELLQDKWASL 649
 Db 619 LEQIWNHTTWMEWDREIDNTHLYTLIEESONQOEKNEQELLELDKWASL 669

RESULT 4

US-11-014-842A-25

; Sequence 25, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBECQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR FILING DATE: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patent In Ver. 3.3

; SEQ ID NO 25

; LENGTH: 681

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-25

Query Match 79.3%; Score 2756.5; DB 7; Length 681;

Best Local Similarity 79.4%; Pred. No. 2.6e-246;

Matches 517; Conservative 60; Mismatches 53; Indels 21; Gaps 8;

Qy 3 LMTVYGVVPWKATTLTFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 62
 Db 34 LMTVYGVVPVREATTTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 93
 Qy 63 NMWKNNVQEHEDIISLWDSLPKVCVLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 121
 Db 94 NMWKNNVQEHEDIISLWDSLPKVCVLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 149
 Qy 122 QRGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNVT 181
 Db 150 MMEGEIKNCSFYITTSIRNKVKKEYALFNRLDVPV---KN-TSNTKYLINCNVT 205
 Qy 182 QACPKVSFPIPIHYCTPTGTGALLKCNKDKFNGTGPCTNVSTVQCTHGIRPVVSTQLLN 241
 Db 206 QACPKVSFQPIPIHYCVPAAGFAILKCNKNTFNGSGPCTNVSTVQCTHGIRPVVSTQLLN 265
 Qy 242 GSLAEEVIRSEFTNNAKIIIVQLNVSVINCTRNPNHTRKRVTLGPRVWTTTGELL 301
 Db 266 GSLAEEVIRSEFTNNAKIIIVQLNVSVINCTRNPNHTRKRVTLGPRVWTTTGELL 325

Qy 302 GNIRQAHCHNSRAQWNNTLQOIATTLREQFNKTIQAFNQSSGGDPEIVMHSFNCGEFFY 361
 Db 326 GDIRQAHCHNSRAKWNNTLQOIVIKLREKFNKTIQAFNQSSGGDPEIVMHSFNCGEFFY 385
 Qy 362 CNSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRKQIINRWQVGVKAMALPIK 419
 Db 386 CNTAQLFNSWVAGTNGT-----EGNDIITLPCRKQIINRWQVGVKAMAPPI 437
 Qy 420 GLIRCSSNITGLLTRDGGGNNQTEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPT 478
 Db 438 GQIRCSSNITGLLTRDGGGNNSEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPT 497
 Qy 479 KAKRVVQREKRAVGMGLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
 Db 498 RAKERTVQREKRAVG-ICAVFLGFLGAAGSTMGASVTLTVOARQLLSGIVQOQNLLRA 556
 Qy 539 IKAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCGSKLICCTTAVPWNASWNT 598
 Db 557 IEAQOHLQLLTWGIKQIARILAVERYLKQOQLLGFPGCGSKLICCTTAVPWNASWNTS 616
 Qy 599 LDOIWNNTWMEWDREIDNTHLYTLIEESONQOEKNOQELLQDKWASL 649
 Db 617 VDDIWNNTWMEWDREIDNTHLYTLIEESONQOEKNEKELLELDKWASL 667

RESULT 5

US-11-014-842A-27

; Sequence 27, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBECQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR FILING DATE: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patent In Ver. 3.3

; SEQ ID NO 27

; LENGTH: 869

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-27

Query Match 79.3%; Score 2756.5; DB 7; Length 869;

Best Local Similarity 79.4%; Pred. No. 3.7e-246;

Matches 517; Conservative 60; Mismatches 53; Indels 21; Gaps 8;

Qy 3 LMTVYGVVPWKATTLTFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 62
 Db 34 LMTVYGVVPVREATTTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 93
 Qy 63 NMWKNNVQEHEDIISLWDSLPKVCVLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 121
 Db 94 NMWKNNVQEHEDIISLWDSLPKVCVLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 149
 Qy 122 QRGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNVT 181
 Db 150 MMEGEIKNCSFYITTSIRNKVKKEYALFNRLDVPV---KN-TSNTKYLINCNVT 205
 Qy 182 QACPKVSFPIPIHYCTPTGTGALLKCNKDKFNGTGPCTNVSTVQCTHGIRPVVSTQLLN 241
 Db 206 QACPKVSFQPIPIHYCVPAAGFAILKCNKNTFNGSGPCTNVSTVQCTHGIRPVVSTQLLN 265

Db 150 MMEGEIKNCSPYITTSIRNKVKKEYALFNRLDVVPV---KN-TSNTKYRLISCNTSVIT 205
Qy 182 QACPKVSEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPWSVQTLN 241
Db 206 QACPKVSEPIPIHYCVFAGPAILKCNCKKNGTGPCTNVSTVQCTHGIRPWSVQTLN 265
Qy 242 GSLAEVIVIRSEFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPGRVWTTGELL 301
Db 266 GSLAEEDIVIRSEFTDNVKTIIIVQLNESVVINCTRPNNAAEL-----DKWASAA--- 316
Qy 302 GNIRAHNCISRAOWNNTLOQIATTLRQFGNKTIAFNQSSGGDEIIVHSHFNCGGEPFY 361
Db 317 ---RQAHNCISRAOWNNTLOQIATTLRQFGNKTIAFNQSSGGDEIIVHSHFNCGGEPFY 373
Qy 362 CNSTQLFNSANNVT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPK 419
Db 374 CNTAQLFNSVNWAGTNGT-----EGNDIITLPCRKIQIINRWQVGVKAMYPK 425
Qy 420 GLIRCSSNITGLLLTRDGGNGOT--TEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 478
Db 426 GQIRCSSNITGLLLTRDGGNGOT--TEIFRPGGDMRDNRSELYKYKVVRIEPIGVAPT 485
Qy 479 KAKRVVQREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNNLLRA 538
Db 486 RAKRTVQREKRAVG--IGAVFLGFLGAAGSTMGAASTVLTVOARQLLSGIVQOQNNLLRA 544
Qy 539 IKAQHLLQTLVWGIKQIARILAVERYLKDQQLGFGWCSGKLICTTAVPWNASWSNKT 598
Db 545 IEAQNNMLRLTVWGIKQIARVLALELYRLDQQLGFGWCSGKLICTTSVPWNVSNK 604
Qy 599 LQIANNMTMWEDEIDNYTHLYITLIEESQNOEKQOELLQDKWASL 649
Db 605 VDDIANNMTMWEDEIDNYTHLYITLIEESQNOEKQOELLQDKWASL 655

RESULT 8

US-11-014-842A-33
; Sequence 33, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBESQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014.842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-33

Query Match 72.2%; Score 2509.5; DB 7; Length 613;
Best Local Similarity 72.6%; Pred. No. 1.5e-223;
Matches 472; Conservative 49; Mismatches 42; Indels 87; Gaps 5;
Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 93
Qy 63 NWKNNMVQMHEDIISLWDSLSKPCVKLTPLCVTLNCTDLNNTNTTSLTSIIVWQ 122
Db 94 NWKNNMVQMHEDIISLWDSLSKPCVKLTPLCVTLNCTDLNNTNTTSLTSIIVWQ 129

Qy 123 RGKGMNCNCFNITTSIRDKVQREYALFYKLDVEPIDDNKNNTNTNTKYRLINCMNTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSPEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPWSVQTLN 242
Db 139 ACPKVSPEPIPIHYCVFAGPAILKCNCKKNGTGPCTNVSTVQCTHGIRPWSVQTLN 198
Qy 243 SLAEVIVIRSEFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPGRVWTTGELL 302
Db 199 SLAEEDIVIRSEFTDNVKTIIIVQLNESVVINCTRPNNHTRKRVTLGPGRVWTTGELL 258
Qy 303 GNIRAHNCISRAOWNNTLOQIATTLRQFGNKTIAFNQSSGGDEIIVHSHFNCGGEPFY 362
Db 259 DIRAHNCISRAOWNNTLOQIATTLRQFGNKTIAFNQSSGGDEIIVHSHFNCGGEPFY 318
Qy 363 NSTQLFNSANNVT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPK 420
Db 319 NTAQLFNSVNWAGTNGT-----EGNDIITLPCRKIQIINRWQVGVKAMYPK 370
Qy 421 LIRCSSNITGLLLTRDGGNGOT--TEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 479
Db 371 QIRCSSNITGLLLTRDGGNGOT--TEIFRPGGDMRDNRSELYKYKVVRIEPIGVAPT 430
Qy 480 KAKRVVQREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNNLLRAI 539
Db 431 AKRTVQREKRAVG--IGAVFLGFLGAAGSTMGAASTVLTVOARQLLSGIVQOQNNLLRAI 489
Qy 540 KAOHLLQTLVWGIKQIARILAVERYLKDQQLGFGWCSGKLICTTAVPWNASWSNKT 599
Db 490 EAQNNMLRLTVWGIKQIARVLALELYRLDQQLGFGWCSGKLICTTSVPWNVSNKSV 549
Qy 600 DQIANNMTMWEDEIDNYTHLYITLIEESQNOEKQOELLQDKWASL 649
Db 550 DDINNMTMWEDEIDNYTHLYITLIEESQNOEKQOELLQDKWASL 599

RESULT 9

US-11-014-842A-35
; Sequence 35, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBESQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014.842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-35

Query Match 72.2%; Score 2509.5; DB 7; Length 801;
Best Local Similarity 72.6%; Pred. No. 2.1e-223;
Matches 472; Conservative 49; Mismatches 42; Indels 87; Gaps 5;
Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 93

Qy 63 NMWKNMVEQMHEDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 94 NMWKNMVDQMHEDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 129
Qy 123 RGKEMRNCSPNITTSIRDKVQREVALFYKLDVEPIIDNNKNTTNTKYRLINCNSTVITQ 182
Db 130 -----NCNNTSVITQ 138
Qy 183 ACQKVSFPIPIHYCTPTGTFALLKNDKFGTGTCTNNVSTVQCTHGRPVVSTOLLNG 242
Db 139 ACQKVSFQPIPIHYCVAGFALLKNNKTNGSGFCTNNVSTVQCTHGRPVVSTOLLNG 198
Qy 243 SLABEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
Db 199 SLABEDIVIRSEDFDNNVKTIIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 258
Qy 303 NIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAFNQSSGGDPEIYVHNSFNCGGEFFYC 362
Db 259 DIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAFNQSSGGDPEIYVHNSFNCGGEFFYC 318
Qy 363 NSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRILQIINRWVGVKAMVALPIK 420
Db 319 NTAQLFNSWVAGTNGT-----EGNDIITLQCRILQIINRWVGVKAMVALPIK 370
Qy 421 LIRCSSNITGLLTRDGGNGT--TEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPT 479
Db 371 QIRCSSNITGLLTRDGGNGT--TEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPT 430
Qy 480 AKRRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 539
Db 431 AKRRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 489
Qy 540 KAOQHLLQLTQWGIKQLOARILAVERYLKDQQLLGFVGCSCGLICTTAVPWNASWSNKT 599
Db 490 EAQONMLRLTQWGIKQLOARILAVERYLKDQQLLGFVGCSCGLICTTAVPWNASWSNKT 549
Qy 600 DOIWNMTWMEWDREIDNYTHLYTLIEESONQOEKNOELLQDKWASL 649
Db 550 DOIWNMTWMEWDREIDNYTHLYTLIEESONQOEKNOELLQDKWASL 599

RESULT 10

US-11-022-562-219
; Sequence 219, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-219

Query Match 71.6%; Score 2489; DB 7; Length 854;
Best Local Similarity 70.4%; Pred. No. 1.8e-221;
Matches 459; Conservative 73; Mismatches 100; Indels 20; Gaps 6;
Qy 2 NLWVTVYGVPMWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 61
Db 32 NLWVTVYGVPMWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 91

Qy 62 FMWKNMVEQMHEDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWE 121
Db 92 FMWKNMVDQMHEDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWE 147
Qy 122 ORKGEWRNCSPNITTSIRDKVQREVALFYKLDVEPIIDNNKNTTNTKYRLINCNSTVIT 181
Db 148 NNNTSDMKNSFNATTEVTDKIRKENALFYTLIDIVPLDENQ---NNSNYRLINCNSTSKVT 204
Qy 182 QACPKVSFPIPIHYCTPTGTFALLKNDKFGTGTCTNNVSTVQCTHGRPVVSTOLLN 241
Db 205 QACPKVSFPIPIHYCAPAGYALKCNNTFNGTGPCNNVSTIQTCTHGRPVVSTOLLN 264
Qy 242 GSABEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGIL 301
Db 265 GSABEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGIL 324
Qy 302 GNTROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAFNQSSGGDPEIYVHNSFNCGGEFFY 361
Db 325 GDIROAHCHNISRAQWNTLQOIVKIRKFNKTIAFNQSSGGDPEIYVHNSFNCGGEFFY 384
Qy 362 NSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRILQIINRWVGVKAMVALPIK 419
Db 385 CNTSSLFNNTYRPTWPNGT-----ESNSTITLQCRILQIINRWVGVKAMVALPIK 436
Qy 420 GLIRCSSNITGLLTRDGGNGT--TEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAP 477
Db 437 GKITCKSNITGLLTVRDGGNGNTATEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAP 496
Qy 478 TKARRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 537
Db 497 TGARRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 555
Qy 538 AKAQHLLQLTQWGIKQLOARILAVERYLKDQQLLGFVGCSCGLICTTAVPWNASWSNKT 597
Db 556 AKAQHLLQLTQWGIKQLOARILAVERYLKDQQLLGFVGCSCGLICTTAVPWNASWSNKT 615
Qy 598 TLDOIWNMTWMEWDREIDNYTHLYTLIEESONQOEKNOELLQDKWASL 649
Db 616 SQADIWNMTWMEWDREIDNYTHLYTLIEESONQOEKNOELLQDKWASL 667

RESULT 11

US-11-014-842A-37
; Sequence 37, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR FILING DATE: 2003-06-20
; PRIOR FILING DATE: 2003-06-20
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 37
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-37

Query Match 69.7%; Score 2421.5; DB 7; Length 601;
Best Local Similarity 71.1%; Pred. No. 1.9e-215;
Matches 462; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
Qy 3 LWTVTVYGVPMWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 62

Db 34 LWVTVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 93
Qy 63 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTNTTSLIIVVWEQ 122
Db 94 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTL----- 129
Qy 123 RGKGBMRNCNFIITTSIRDVKVOREVALFYKLDVEPIDDNKNTNTNTKYRLINCVTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGTCTNVSTVQCTHGRPVVSTOLLNG 242
Db 139 ACPKVSFPIPIHYCVPAGFAILKCNKNTFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 198
Qy 243 SLAEDEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 199 SLAEDEVIRSEDFTDNVKTIIVQLNVSVINCTRPNNAAEL-----DKWASAA----- 248
Qy 303 NIROAHNCISRAQWNTLQOIATTLREOFNGKNTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 249 --ROAHNCISRAQWNTLQOIVIKLREKFRNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 306
Qy 363 NSTOLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 420
Db 307 NTAQLFNSWNVAGTNGT-----EGNDIITLCRIKQIINRWQVVGKAMVALPIKG 358
Qy 421 LIRCSSNITGLLITRDGGGENQT--TEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTK 479
Db 359 QIRCSSNITGLLITRDGGNSTETETETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTR 418
Qy 480 AKRRVQREKRAVGMGLAMFLGAGSTMGATSMALTVOAROLLGIVQOQNNLLRAI 539
Db 419 AKRRVQREKRAVG--IGAVFLGFLGAGSTMGATSMALTVOAROLLGIVQOQNNLLRAI 477
Qy 540 KAOQHLLQLTWVGIKQLQARILAVERYLKDOQLLGFWCGSKGLICTTAVPNNASWNSKTL 599
Db 478 EAQNNMLRLTWVGIKQLQARVLALEERYLDQOQLMGINGCGSKGLICTTSVPNNVSNKSV 537
Qy 600 DQIWNMTWMEWDREIDNTHLYTLIEESQOQKQOELLQLDKWSL 649
Db 538 DDINNMTWMEWEREIDNTHLYTLIEESQOQKQOELLQLDKWSL 587

RESULT 12
US-11-014-842A-39
; Sequence 39, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014, 842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 39
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-39

Query Match 69.7%; Score 2421.5; DB 7; Length 789;
Best Local Similarity 71.1%; Pred. No. 2.8e-215;

Matches 462; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
Qy 3 LWVTVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 62
Db 34 LWVTVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 93
Qy 63 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTNTTSLIIVVWEQ 122
Db 94 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTL----- 129
Qy 123 RGKGBMRNCNFIITTSIRDVKVOREVALFYKLDVEPIDDNKNTNTNTKYRLINCVTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSFPIPIHYCTPTGTFALLKNDKFKNGTGTCTNVSTVQCTHGRPVVSTOLLNG 242
Db 139 ACPKVSFPIPIHYCVPAGFAILKCNKNTFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 198
Qy 243 SLAEDEVIRSENFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 199 SLAEDEVIRSEDFTDNVKTIIVQLNVSVINCTRPNNAAEL-----DKWASAA----- 248
Qy 303 NIROAHNCISRAQWNTLQOIATTLREOFNGKNTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 249 --ROAHNCISRAQWNTLQOIVIKLREKFRNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 306
Qy 363 NSTOLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 420
Db 307 NTAQLFNSWNVAGTNGT-----EGNDIITLCRIKQIINRWQVVGKAMVALPIKG 358
Qy 421 LIRCSSNITGLLITRDGGGENQT--TEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTK 479
Db 359 QIRCSSNITGLLITRDGGNSTETETETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTR 418
Qy 480 AKRRVQREKRAVGMGLAMFLGAGSTMGATSMALTVOAROLLGIVQOQNNLLRAI 539
Db 419 AKRRVQREKRAVG--IGAVFLGFLGAGSTMGATSMALTVOAROLLGIVQOQNNLLRAI 477
Qy 540 KAOQHLLQLTWVGIKQLQARILAVERYLKDOQLLGFWCGSKGLICTTAVPNNASWNSKTL 599
Db 478 EAQNNMLRLTWVGIKQLQARVLALEERYLDQOQLMGINGCGSKGLICTTSVPNNVSNKSV 537
Qy 600 DQIWNMTWMEWDREIDNTHLYTLIEESQOQKQOELLQLDKWSL 649
Db 538 DDINNMTWMEWEREIDNTHLYTLIEESQOQKQOELLQLDKWSL 587

RESULT 13
US-11-022-562-340
; Sequence 340, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-340

Query Match 32.8%; Score 1140; DB 7; Length 879;
Best Local Similarity 38.8%; Pred. No. 7.2e-97;

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Mar-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: 09/131,551
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11

Query Match 18.8%; Score 653; DB 7; Length 145;
Best Local Similarity 87.5%; Pred. No. 5.2e-53;
Matches 119; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
Qy 514 SMALTQARQLSGIVQOQNNLLRAIKAOQHLLQLTWGKIQARILAVERYLKDQQLL 573
Db 2 SLTLTVQARQLSGIVQOQNNLLRAIEAQHLLQLTWGKIQARVLAVERYLRDQQL 61
Qy 574 GFWCGSGKLICTTAVPWNASNSKTLDOIWNMTTWMDREIDNYTHLYTLIESQNOQ 633
Db 62 GIWCGSGKLICTTAVPWNASNSKSLDIWDMTWQWREIDNTNTIYTLLESQNOQ 121
Qy 634 EKNQQLQLDKWASL 649
Db 122 EKNEQLLELDKWASL 137

Search completed: March 7, 2006, 17:57:10
Job time : 25.8879 secs

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